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(54) Title: UNIVERSAL PRIMERS FOR WILDLIFE IDENTIFICATION

(57) Abstract: The invention provides novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin and a method for identification of the specific animal from a given biological sample.



**WO 02/077278 A1**

## UNIVERSAL PRIMERS FOR WILDLIFE IDENTIFICATION

### TECHNICAL FIELD

The invention relates to the identification of novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin at species and sub-species sources. The invention also provides a method for the identification of fragments on mitochondrial cytochrome b gene in biological material of unknown origin.

### BACKGROUND ART

A large number of studies in evolutionary biology utilize phylogenetic information obtained from mitochondrial cytochrome b gene. It has been identified a potent molecule to distinguish the phylogenetic depth of different lineages to family, genus and species in molecular taxonomy<sup>1-66</sup>. A vast database of the sequences of cytochrome b gene of different animal species has accumulated in public databases such as GenBank, NCBI (<http://www.ncbi.nlm.nih.gov>) etc. We have utilized this capacity of cytochrome b gene in establishing the identity of the origin of animal parts and product to its family, genus and species sources. The technique developed is based on a pair of universal primer that can amplify a small fragment of cytochrome b gene from a vast range of animal species.

Establishing identity of confiscated animal parts and products is a great challenge to law enforcement agencies because none of the methods available till date is too efficient to reveal the identity of animal remains beyond a reasonable doubt. Morphological markers, described for certain species allow the identification of complete specimen of animals<sup>67</sup>. However, a complete specimen is confiscated very rarely by the investigation agencies; therefore, these marker are not practical in wildlife forensics. The biochemical traits such as the bile characteristics<sup>68</sup> blood heam analysis<sup>69,70</sup> etc. have also been employed in wildlife forensic for identification of individual species. The difficulty of these markers are that these markers are limited in number and are rarely found in their natural forms in which these were originally described as the characteristic of a particular species.

The molecular approaches such as micro-satellite based identification<sup>71</sup>, Restriction fragment length polymorphism analysis of mitochondrial genes or PCR based species specific STS markers require the prior information of the species to establish the identity<sup>72,73</sup>. These methods also need a significant amount of DNA material to be analysed. We may not have the prior information about the species origin of confiscated animal parts and product in forensics. therefore, these methods are not really useful and

practical in wildlife identification. The technique invented by us is universal, therefore does not require any background information to establish the identity of any unknown confiscated remains at family, genus and species sources. Being a PCR based procedure it can be applied with trace amount of any biological material. Because the amplicon length is small (472 bp); therefore, it can work perfectly with the mutilated remains, which are commonly seized by the crime investigation agencies. It does not require the large amount of genetic material i.e. DNA to be analyzed to establish the identity, hence, can detect a minute amount of adulteration in food products. The procedure described is simple and very fast. Due to the said advantages, the procedure invented by us is most suited for forensic wildlife identification.

### OBJECTS OF THE INVENTION

The main object of the invention is to identify a fragment on mitochondrial cytochrome b gene capable of significantly discriminating among various evolutionary lineages of different animal species.

Another object is to identify a fragment on mitochondrial cytochrome b gene which is flanked by the highly conserved sequences at a vast range of animal species.

Yet another object is to detect a fragment on mitochondrial cytochrome b gene which is polymorphic inter-specifically, but monomorphic at intra species sources.

Still another object is to develop the universal primers to amplify the fragment on mitochondrial cytochrome b gene using polymerase chain reaction.

Another object is to develop a PCR protocol that works universally with DNA template of any unknown origin (i.e. all the animal species).

Yet another object is to provide a universal method for identification of species of analyzed material (i.e. the DNA isolated from confiscated animal remain of unknown origin) using the public databases such as GenBank, NCBI etc.

Still another object is to provide a universal method of animal identification to establish the crime with the criminal beyond a reasonable doubt.

Another object is provide a universal method to establish the identity of biological materials such as skin, horns etc confiscated from animal poachers, if it is that of an endangered species.

Yet another object is to provide a universal method for establishment of the identity of confiscated animal parts and products of endangered animal species for the purpose of production of molecular evidence of animal hunting and related crime in the court of law, so that the human violation to the wildlife resources could be controlled.

Still another object is to provide a universal technique to have an idea of the geographical location of the commitment of wildlife crime based on the haplotype of poached animal identified by the universal primer invented.

Another object is to provide a universal technique of animal identification to detect the adulteration of animal meat/products in vegetarian food product for the purpose of food fortification, by the food fortification agencies.

Yet another object is to provide a universal technique for detection of the origin of blood or blood stains etc collected from the scene of crime related to offences such as murder, rape etc, in order to establish the origin of blood found at scene of crime when it sounds as if criminals have wontedly spread the blood of an animal at the scene of crime, to confuse the crime investigation agencies and forensic scientists with human blood.

Another object is to invent and authenticate a universal technique that can be converted to a (a) 'MOLECULAR KIT' and (b) 'DNA CHIPS' based application to meet the requirements of above objectives.

## 15 SUMMARY OF THE INVENTION

Accordingly, the invention provides novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin

## DETAILED DESCRIPTION OF THE INVENTION

20 Keeping in view the above objectives, the cytochrome b gene sequences (1140 bp) of 221 distantly related animal species (listed in Table 1) representing various families were obtained from public database NCBI (<http://www.ncbi.nlm.nih.gov>). These sequences were aligned using the software *Clustal X*(1.8)(NCBI, USA) and a fragment (of 472 bp, alignment shown in Table 2) of gene was identified which had all the features mentioned above under column 1, 2 and 3 of sub-heading 'Objectives of invention'. As for the identity of this fragment we would like to mention that it includes the nucleotides between 398 to 869 in *Antelope cervicapra* and *Felis catus*; however, 399 to 870 in *Homo sapiens sapiens* species. Except at few positions (marked as star (\*)) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, giving rise to their unique molecular signature. These molecular signatures are characteristic of its species and form the basis of revealing the identity of the biological material of an unknown animal origin by the procedure invented by us. Considering *Antelope cervicapra* as a representative species, the sequence of this fragment is mentioned herewith:

Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antelope cervicapra*:



“taccatgaggacaaatatcttttgaggagcaacagtcacccaatctctttcagcaatcccatacatcggtacaaacctagtaga  
atgaatctgaggagggttctcagtagataaagcaacccttaccgatttttcgcttccactttatctctccattatcattgcagccctt  
accatagtacacctactgtttctccagaaacaggatccaacaaccccacaggaatctcatcagacgcagacaaaattccattccac  
ccctactacactatcaaaagatactctaggagctctactattaattttaaccctcatgcttctagtctctattctcaccggacctgctggag  
5 acccagacaactatacaccagcaaacccacttaatacacccccacatatcaagcccgaatgatacttctatttgcatacgcaatcct  
ccgatcaattcctaacaactaggagg”.

A pair of universal primer was designed to amplify this fragment in polymerase chain reaction (PCR). These primers were named as ‘mcb398’ and ‘mcb869’ because of its property to amplify a region of mitochondrial cytochrome b gene between nucleotides 398  
10 to 869 of *Antilope cervicapra*, a representative animal species for this invention. We took this animal species as representative species because the idea of developing such a novel primers came in the mind of inventors while they were working on the genome of this animal in Centre for Cellular and Molecular Biology, Hyderabad, India. These primers work universally because its 3’ end are highly conserved amongst a vast range of animal  
15 species (shown in Table 2). As mentioned above, the DNA fragment (sequence of which is shown above) targeted by these primers is highly polymorphic inter-specifically; however, it is monomorphic among the individual of same species (Tables 6, 7a, 7b, 7c, 7d and 8, respectively). These unique features of the targeted region enable these primers to generate the molecular signatures of an individual species; thereby, enabling them to differentiate  
20 amongst the animals of different species (see in Figure 1c). The variation within the fragment amplified by these primers increase with increasing distances of evolutionary lineages of two animals (Table 8). These unique features of the fragment amplified by the universal primers ‘mcb398’ and ‘mcb869’ invented by the applicants fulfill the objectives of invention.

25 Thus, the primers invented by us can generate the molecular signature from any biological material of unknown animal origin, which actually is the characteristic of its family, genus and more precisely, the species. When these signatures are compared *in-silico* with the signatures already available in public databases (viz., GenBank, NCBI database etc) using ‘BLAST software’<sup>73</sup>, it indicates identity of the family, genus or species of the analyzed  
30 material, which in turn is confirmed practically by comparing with the reference animals of the revealed family, genus or species, by including them in the further analysis by the primers ‘mcb398’ and ‘mcb869’. The complete procedure involved in the *analyses* (the word, ‘analyses’ should be understood with the stepwise procedure to establish the identity of the biological remain of any unknown animal origin for the aims mentioned in columns

1-13 under sub-heading 'Objectives of invention') is briefed under 'Examples 5 and 6, respectively, as well as illustrated in Figures 1a, 1b and 1c, respectively.

### BRIEF DESCRIPTION OF DRAWING AND TABLES

5 **Figure 1a.** Illustration of the step-wise procedure involved in *analyses*. The unknown biological material i.e. 'adil.flesh' refers to the confiscated skin mentioned in 'Example 6'. The arrow marks indicate the stepwise procedure involved. The brief description of Figure 1a is as follows:

The biological material i.e. the confiscated skin 'adil.flesh' was subjected to DNA isolation using the standard procedures<sup>74</sup>. The DNA obtained was amplified using the primers  
10 'mcb398' and 'mcb869' in PCR, fractionated in 2% (w/v) agarose gel, visualized and photographed under UV light using Gel Documentation System (Syngene, USA). The lane 'M' shown in the photograph represents the molecular weight marker (Marker XIII, Boehringer mannheim). Lane 1 shows the PCR amplicon (472 bp) obtained from 'adil.flesh' using primers 'mcb398' and 'mcb869'. The PCR amplicon obtained were  
15 sequenced at both the strand using "ABI Prism 3700 DNA Analyzes, PE-Applied Biosystems). The chromatogram shows the sequences (about 80 bp long, i.e. between 150-230 bp of sequence (328 bp), revealed from the PCR product of 472 bp length) obtained from 'adil.flesh'.

**Figure 1b.** Illustrates the further steps involved in *analyses*. The sequence (328 bp)  
20 revealed from 'adil.flesh' was subjected to homology search in *nr* (i.e. *non-redundant*) database of National Centre for Biological Information (NCBI), USA. The sequences producing significant alignments are shown along with its bits score and E values. It indicates the extent of homology amongst the sequence enquired (i.e. the 328 bp sequence from adil.flesh) and the sequences registered in *nr* database of NCBI. BLAST analysis  
25 revealed the highest homology of the sequence revealed from 'adil.flesh' with the sequence of *Panthera pardus* (gene bank registration number 'AY005809'), indicating the identity of adil.flesh as that of a leopard (*Panthera pardus*) origin. Figure 1b further illustrates the multiple alignments of the sequences obtained from reference animals (listed in Table 5) along with the sequence obtained from 'adil.flesh'. The sequences of  
30 'adil.flesh' is similar to the sequences of 'gz1L' further confirming the identity of the source of confiscated remain 'adil.flesh' as that of a *Panthera pardus* origin.

**Figure 1c** illustrates the NJ-tree (Neighbor Joining tree) constructed using CLUSTAL X (1.8) from the sequences revealed from 'adil.flesh' and reference animals listed in Table 5.

The animals belonging to similar species cluster together; however, the animals of different species group in different clusters. The confiscated material under investigation (i.e. 'adil.flesh') clusters with 'gz1L' (i.e. the known normal leopard '*Panthera pardus*') indicating the identity of the species of 'adil.flesh' as that of a *Panthera pardus* source.

5 **Figure 2** shows the Agarose gel electrophorogram showing the PCR amplicons (472 bp) obtained from the reference animals of family felidae listed in Table 5, using universal primers 'mcb398 and 'mcb869'. Description of different lanes is as follows:

Lanes 1-21: The PCR profiles of the animals 1-21, respectively, listed in Table 5.

10 Lane 22: The PCR profiles of DNA isolated from confiscated skin of unknown animal origin 'i.e. adil.flesh'

Lane 23: Negative control (no DNA)

Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)

**Figure 3.** Shows PCR amplicons obtained from animals listed in Table 9. The primers used in PCR are 'AFF' and 'AFR'. The description of different lanes shown is as follows:

15 Lane 1-4: The PCR profiles of animals 1-4, respectively, listed in Table 9, showing amplicons of 354 bp.

Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)

20 **Figure 4.** Shows PCR amplicons obtained from animals listed in Table 12. This experiment demonstrates the universal nature of our primers among a vast range of animal species. Description of different lanes shown is as follows:

Lanes 1-23: The PCR profiles of the animals 1-23, respectively, listed in Table 12. The PCR product of 472 bp is amplified universally from all the animal species analyzed.

Lane 24: Negative control (no DNA)

Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)

25 **Table 1.** List of 221 animal species used for *In-silico* analysis to design the universal primers 'mcb398' and 'mcb869'. Table also demonstrate the 'P,S scores' of 'mcb398' and 'mcb869' for different templates. The descriptions of various symbols used in this table are as follows:

Symbol (#) refers to Number

30 Symbol (\*) refers to the animal species which is either protected species (listed in Wildlife (Protection) Act , 1972 (Central Act NO 53 of 1972), or an endangered/rare animal species

Symbol (<sup>S</sup>P,S/F) refers to Probability of match and Stability of match of primer 'mcb398' with different templates (i.e. the cytochrome b gene from different species origin). A higher P, S score refers to the higher probabilities of significant amplification of specific

template by the primer. It is calculated by *Amplify (1.2)* software.

Symbol ( $\Psi$ P,S/R) refers to Probability of match and Stability of match of primer 'mcb869' with different templates. A higher P,S score refers to the higher probabilities of significant amplification of specific template by the primer. It is calculated by *Amplify (1.2)* software.

5 **Table 2.** Multiple sequence alignment of 472 bp fragment of mitochondrial cytochrome b gene (identified by inventors to fulfill the requirements of column 1, 2 and 3 mention under sub-heading 'Objectives of invention') of 221 animal species listed in Table 1. Alignments also show the binding sites for universal primers 'mcb398' and 'mcb869'. The symbol (\*) refers to the nucleotide bases which are conserved amongst 221 animal species  
10 listed in Table 1). The alignments have been done using software *CLUSTAL X (1.8)*. The nucleotide positions that are unmarked are variable amongst 221 animal species analyzed. These variable sites together constitute the molecular signature of an individual species, giving rise to molecular basis of species identification by our primers.

**Table 3.** Results of the blast analysis of the sequence revealed from 'adil.flesh' in 'mito' database of NCBI. It shows the most significant alignment of cytochrome b sequence (328 bp) revealed from confiscated skin piece 'adil.flesh' with *felis catus* cytochrome b gene sequence (genbank registration number NC\_001700.1, bits score 365, E value, e-101) registered in NCBI database (bits score 365 and E value e-101). It gives an indication that the species of analyzed material belongs to family felidae. It also fulfills the requirements  
20 of column 6 mention above under sub-heading 'Objectives of invention'.

**Table 4.** Results of the blast analysis of the sequence revealed from 'adil.flesh' in 'nr' database of NCBI. It shows the most significant alignment of cytochrome b sequence (328 bp) revealed from confiscated skin piece 'adil.flesh' with *Panthera pardus* cytochrome b gene sequence (genbank registration number AY005809, bits score 603, E value, e-170)  
25 registered in NCBI database. It gives an indication that the species of analyzed material belongs to *Panthera pardus* origin. It also fulfills the requirements of column 6 mention above under sub-heading 'Objectives of invention'.

**Table 5.** Reference animal belonging to family felidae selected for comparison with 'adil.flesh' to confirm the findings of BLAST analysis results of which are mentioned in  
30 Table 3 and 4, respectively. The animals listed in SN. 1-21 represent different species of family felidae. SN. 22 and 23 are primate species taken for out-group comparisons.

**Table 6** Multiple sequence alignments of cytochrome b sequences (328 bp) revealed from 'adil.flesh' and reference animals listed in Table 5. The positions that have a common nucleotide in all the animal species under investigation are shown with a star (\*) mark;

however, the positions that are variable in any of the animals under investigation are unmarked. The nucleotides at these positions constitute the molecular signature of an individual species, which are unique and highly specific for its species. These signatures are the molecular basis of identification of individual animal species using our primers 'mcb398' and 'mcb869'.

**Table 7** (Tables 7a, 7b, 7c and 7d). The comparison of the molecular signatures of different animal species investigated along with 'adil.flesh', the confiscated skin of unknown animal origin. This table demonstrates the variable positions (i.e. the positions which are not marked with star (\*) symbol in Table 6), amongst the 328 bp fragment revealed from the animals listed in Table 5. The dot (.) mark represents the presence of the similar nucleotide as listed in lane 1 i.e. the sequence from "adil.flesh" at that position. It demonstrates that the signatures of each species are unique and specific to its species. The molecular signatures of 'adil.flesh' are comparable (except for position 37 which has a transition from 'T' to 'C') to the molecular signature of 'gz1L' i.e. the known leopard '*Panthera pardus*' source, indicating the identity of the source of confiscated skin 'adil.flesh' as that of a leopard '*Panthera pardus*' source. The nucleotide variations (at the positions 153, 198, 223, 264, among the known leopards, (i.e. gz1L, gz2L, and gz3L, respectively)), give an idea about the geographical habitat of each animals. Various studies referring to molecular evolution of different animal species support this hypothesis<sup>75</sup>; however, it could further be confirmed by taking the reference animals from different geographical areas and analyzing by our primers 'mcb 398' and 'mcb869'. If we could generate the database of different haplotypes (i.e. habitat specific molecular signatures) of the animal species, it would also enable our primers to reveal the geographical location of the commitment of wildlife crime.

**Table 8.** Percent similarity matrix calculated by pair-wise comparisons of nucleotide sequences aligned (illustrated in Table 6). The cytochrome b gene sequence of DNA isolated from confiscated material had maximum similarity (99.7% and 98.2%, with the lineages of animals 'gz2L' and 'gz3L', respectively) with the sequences obtained from known normal leopard source, indicating its identity as that of a leopard origin. The similarity matrix has been calculated using the software *PHYLIP* (3.5).

**Table 9.** Animals selected for validation of minimum P,S score for efficient amplification of cytochrome b gene of different origin by the primers 'mcb398' and 'mcb869'. P,S score of primers 'AFF' and 'AFR' for these animals are shown.

**Table 10.** BLAST analysis of primers 'mcb398' in *nr* database of NCBI. It demonstrates

that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer

**Table 11.** BLAST analysis of primers 'mcb869' in *nr* database of NCBI. It demonstrates

5 that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer.

**Table 12.** Other animal belonging to distantly related animal species, investigated to

10 confirm the universal nature of primers 'mcb398' and 'mcb869'. Gel photograph showing the PCR amplicons from these animals are shown in Figure 4.

The mitochondrial cytochrome b gene has very widely been used in molecular taxonomic studies. It has immense capabilities to reveal different evolutionary lineages of animals in family, genus and species specific manner. It has also been used to classify the population

15 of a particular species according to its demographic distributions<sup>75</sup>. The vast database of cytochrome b sequences of different animal species has accumulated in public databases such as Genbank and NCBI<sup>1-65</sup>. We have explored these unique characteristics of cytochrome b gene to establish the identity of confiscated remains of any unknown animal by inventing a pair of novel primers, 'mcb398' and 'mcb869', that can amplify a small

20 fragment (472 bp) of cytochrome b gene of wide range of animal species in universal manner. These primers work universally because its 3' ends target within a highly conserved region.

The fragment of cytochrome b gene identified had all the features mentioned in columns 1, 2 and 3 listed under sub-heading 'Objective of invention'. We identified this fragment by

25 aligning the cytochrome b gene sequences (1140 bp) of 221 different animal species listed in Table 1. These sequences are publicly available in NCBI DNA databases. These sequences were aligned using the software *CLUSTAL X* (1.8). As mentioned before, the 472 bp fragment of cytochrome b gene identified by us to have the features mentioned in columns 1, 2 and 3 listed under sub-heading 'Objective of invention' includes the

30 nucleotides between 398 to 869 in *Antelope cervicapra* and *Felis catus*; however, 399 to 870 in *Homo sapiens sapiens* species. Except at few positions (marked as star (\*)) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, revealing the identity of the biological material belonging to that of an unknown animal origin by the procedure invented by us. As for identity of this fragment we are

considering *Antilope cervicapra* as a representative species, and the sequence the above fragment of cytochrome b gene of *Antilope cervicapra* is mentioned herewith:

Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra*

“taccatgaggacaaatatcttttgaggagcaacagtcacccaatctccttcagcaatcccatatcggtacaaacctagtaga  
 5 atgaatctgaggagggttctcagtagataaagcaacccttaccgatttttcgcttcactttatctctccatttatcattgcagccctt  
 accatagtacacctactgtttctccacgaaacaggatccaacaacccacaggaatctcatcagacgcagacaaaaatccatccac  
 ccctactacactatcaaagatatcctaggagctctactattaatttaaccctcatgcttctagtctctattctcaccggacctgctggag  
 acccagacaactataaccagcaaacccacttaataacccccacatatcaagcccgaatgatacttctatttgcatacgcaatcct  
 ccgatcaattcctaacaactaggagg

10 Table 2 presents the alignment of the above fragment of cytochrome b gene of 221 animal species. Each species in table 2 has been represented by a unique code, which is decoded in Table 1. We selected these species to represent the vast range of animal families of distant orders. Of 221 species, about 65 were the protected/endangered or rare species listed in Wildlife (Protection) Act , 1972 (Central Act NO 53 of 1972). These species are marked  
 15 with symbol (\*) in Table 1. The NCBI accession number refers to its registration number in NCBI database and the number in superscript represent the reference cited. Based on the aligned cytochrome b sequences of different 221 animal species the primers designed were as follow:

Primers name	Sequence (5'-3')
20 'mcb398'	“TACCATGAGGACAAATATCATTCTG”
'mcb869'	“CCTCCTAGTTTGTTAGGGATTGATCG”

Tables 2, 10 and 11, respectively, demonstrates that the 3' ends of the primers are highly conserved amongst all the animal species analyzed *in-silico* (In total 221 animal species listed in Table 1 and about 500 species listed in Tables 10 and 11, respectively) Also, the  
 25 5' end of the primers were selected within the conserved region of cytochrome b gene to improve the probability and stability of match of the primers to their target sequences (i.e. the above mentioned 472 bp fragment of cytochrome b gene). The primers were thoroughly checked for internal stabilities, loop or dimmer formation using different software viz., 'Amplify (1.2)', 'Primer3' (<http://www.genome.wi.mit.edu/cgi-bin/primer/primer3.cgi>) as well as manually. . We assigned the P,S score (P=Probability of match, S=Stability of match) to the primers for each template using the software *Amplify (1.2)*. The higher scores of P and S ensure a good amplification if all other conditions standard (which are mentioned under 'Example 3') are optimum. The Highest score for  
 30 'mcb398' was 98.63 (i.e. the situation where the primer has perfect match with template);

however, the highest P, S for 'mcb869' was recorded as 98, 68 for a complete match between the primer and template. The lowest P,S score observed for 'mcb398' was 81,50 for species *Talpa europaea* whereas 'mcb869' had a high P, S score for this species (92, 57). The another species which have lowest P, S score for one of the two primers were

5 *Eumeces egregius* and *Equus ainus*. *Eumeces egregius* had P, S score 86, 55 and 73,51 for 'mcb398' and 'mcb869', respectively; however, the P, S score of *Equus ainus* was calculated as 91,61 and 73, 51 for 'mcb398' and 'mcb869', respectively. All other animals had higher P, S scores then the above mentioned species. To ensure that these primers would work efficiently with the DNA template from the animals having the lowest P, S

10 score for one of the primers, we designed an another experiment to validate the lower limits of one of the two primers sufficient for efficient amplification in PCR. We designed an another primer pair (AFF= 5'tagtagaatgaatctgaggagg3' and AFR=5'atgcaaataaggaagtatcattc3'.) having more mis-pairing at their annealing sites (but not at ends), therefore have less internal stability and lower P, S scores for its templates (listed

15 in Table 9). The P,S scores of 'AFF' and 'AFR' were as calculated as low as 41 and 49 for *Platanista gangetica* and *Sus scrofa*. These species were amplified efficiently using the primers 'AFF' and 'AFR' (results shown in Figure 3) (keeping all other conditions standard i.e. the conditions mentioned in 'Example 3'). The lowest P,S scores (86, 55 and 73,51 for species *Eumeces egregius*) for our primers 'mcb398' and 'mcb869',

20 respectively, were higher then the above range of combined P, S scores of 'AFF' and 'AFR' for species *Sus scrofa* (87, 52 and 87, 41), which was efficiently amplified by the primers 'AFF' and 'AFR'. It gives an indication that the primers 'mcb 398' and 'mcb 869' would work with all the species including *Eumeces egregius* efficiently to give rise to the expected product in PCR. This experiment confirmed that the primers 'mcb398' and 'mcb

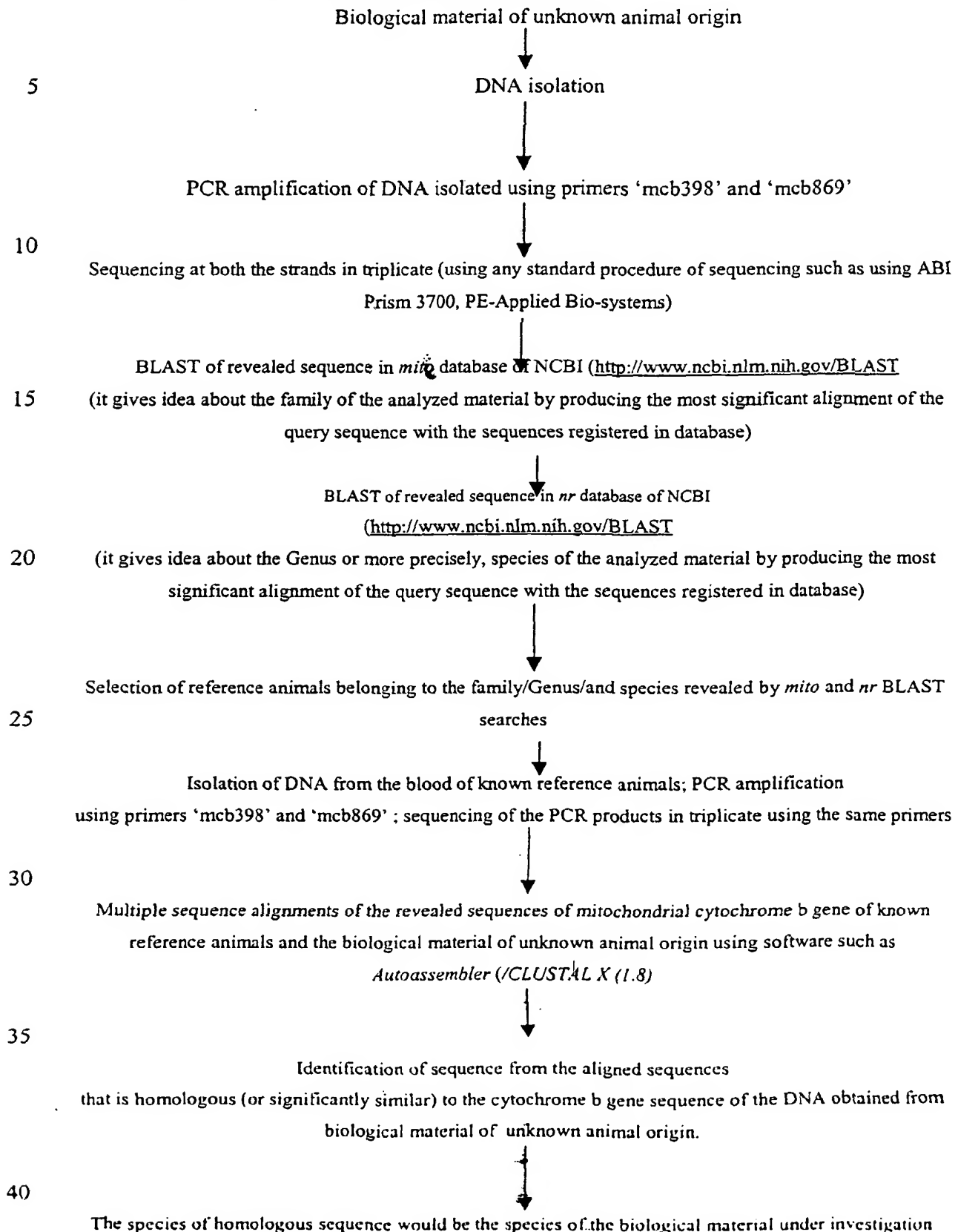
25 869' are capable of amplifying the cytochrome b fragment of most of the animal species in a universal manner.

For further confirmation of universal nature of our primers, we blasted the sequence of our primers against the *mito* and *nr* databases of NCBI using BLAST software. The results of these analyses are shown in Tables 10, and 11, respectively.

30 Finally, the universal nature of the primers was tested in our laboratory with some more animal species listed in Table 12. These primers amplified all the animal species efficiently, giving rise to the band of expected size (472 bp). The results are shown in Figure 4. This experiments substantiated the results of P,S analysis and other *in-silico* analyses to show that the primers 'mcb398' and 'mcb 869' are universal primers.



The flow chart of establishing identity of the species of biological material of unknown animal origin using primers 'mcb398' and 'mcb869'



## Examples

### Example 1

Example for identification of a fragment of cytochrome b gene fulfilling the requirements of columns 1, 2 and 3 mentioned under sub-heading 'Objectives of invention' of heading  
5 'Brief summary of invention'

The cytochrome b molecule has very vastly been used in molecular taxonomic studies. Being a slow evolving gene, It has a tremendous information in its nucleotide sequences to distinguish the animals to their family, genus and species sources<sup>1-65</sup>. A vast database of the sequences of cytochrome b gene of different animal species has accumulated in the *nr*  
10 and *mito* databases of NCBI. We have explored these qualities of cytochrome b gene to establish the identity of confiscated remains of unknown animal origin to its family, genus and species sources. For this purpose, we have identified a fragment of cytochrome b gene which is highly polymorphic inter-specifically, however, it is monomorphic among the individual of same species, therefore it can group the individual of an unknown species  
15 with the known individuals of reference species to which it belongs. In order to amplify this fragment from DNA isolated from any unknown origin, it was necessary that it remain flanked with the highly conserved sequences amongst a vast range of animal families. To identify such a unique fragment within the cytochrome b gene, we aligned the sequences of 221 distantly related animal species (listed in Table 1) representing various families using  
20 software CLUSTAL X (1.8). These sequences were obtained from public database NCBI (<http://www.ncbi.nlm.nih.gov>). The aligned data was examined carefully for the conserved sites amongst all the species included in *in-silico* analysis. We identified a fragment (472 bp) of cytochrome b gene that was fulfilling all the requirements mentioned above and also under column 1, 2 and 3 of sub-heading 'Objectives of invention'.

25 As for the identity of this fragment we would like to mention that it includes the nucleotides between 398 to 869 in *Antelope cervicapra* and *Felis catus*; however, 399 to 870 in *Homo sapiens sapiens* species. Except at few positions marked as star (\*) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, giving rise to their unique molecular signature. These molecular signatures are  
30 characteristic of its species and form the basis of revealing the identity of the biological material of an unknown animal origin by the procedure invented by us. Considering *Antelope cervicapra* as a representative species, the sequence of this fragment is mentioned herewith:

Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antelope cervicapra*

“taccatgaggacaaatatcttttgaggagcaacagtcacccaatctcctttcagcaatcccatacatcggtacaaacctagtaga  
 atgaatctgaggagggttctcagtagataaagcaacccttaccgatttttcgcttccactttatcctcccatttatcattgcagccctt  
 accatagtacacctactgtttctccacgaaacaggatccaacaacccacaggaatctcatcagacgcagacaaaattccattccac  
 ccctactacactatcaaagatatcctaggagctctactattaattttaaccctcatgcttctagtcttctcaccggacctgcttggag  
 5 acccagacaactatacaccagcaaaccacttaatacacccccacatatcaagcccgaatgatacttctatttgcatacgaatcct  
 ccgatcaattcctaacaaactaggagg”

### Example 2:

Example for development of universal primers to amplify the fragment identified mentioned under ‘Example 1’.

A pair of universal primer was designed which has the following features:

1. It targets the fragment identified (mentioned under ‘Example 1’) to amplify it in polymerase chain reaction (PCR).
2. Its 3’ and 5’ ends that are highly conserved (marked as star (\*) in Table 2), amongst a vast range of animal species ensuring the amplification of the fragment mentioned above in a universal manner. The sequencing of the fragment amplified by these primes reveals the molecular signature of the species of analyzed material, which on comparison with the sequences of the known reference animals reveals the identity of the species of unknown biological material under investigation.
3. The  $t_m$  (melting temperature) of both primers was almost similar (about 58 degree centigrade) ensuring the significant annealing of both the primers to its template, therefore significant amplification of targeted region in PCR.
4. The internal stability and P, S, score of the primers were ensured higher while designing it. The possibilities of internal loop formation, dimmer formation etc were also excluded by selecting its sequence uniquely. This ensured that the primer would be a good primer to be used in PCR for amplification of DNA from unknown animal origin.
5. The 3’ end of the primers were ensured to have either ‘G’ or ‘C’ to increase the probability of strong bonding at its 3’ends, which is necessary for efficient amplification of DNA template in PCR. It also strengthens the universal nature of the primer.
6. The sequences of the primers were ensured to be unique so that it does not give rise to non-specific and spurious products in PCR leading to confusion. It improved the efficiency and quality of the technique invented by us.

7. These primers were named as 'mcb398' and 'mcb869' because of its property to amplify a region of mitochondrial cytochrome b gene between nucleotides 398 to 869 of *Antilope cervicapra*, a representative animal species for this invention. We took this animal species as representative species because the idea of developing such a novel primers came in the mind of inventors while they were working on the genome of this animal in Centre for Cellular and Molecular Biology, Hyderabad, India.

8. The sequences of the universal primers invented are as follows:

Primers name	Sequence (5'-3')
'mcb398'	"TACCATGAGGACAAATATCATTCTG"
'mcb869'	"CCTCCTAGTTTGTAGGGATTGATCG"

**Example 3:**

Example for development of universal PCR conditions to ensure the amplification of a template of any unknown origin in PCR, hence strengthening the universal nature of the technique invented by us

The PCR conditions developed had the following unique features:

- 1 These were capable of amplifying the DNA template of any animal origin in an universal manner using the universal primers mentioned under 'Example 2'.
- 20 2. The conditions were selected to ensure the comparable annealing temperature for both the primers i.e. 'mcb398' and 'mcb869'.
3. The PCR conditions standardized herewith are universal; therefore, the possibility of PCR failure with a template of unknown origin due to non-standard conditions is excluded. It ensures the universal nature of our technique to be used in wildlife forensics.
- 25 4. The universal conditions mentioned above are:

Amplification reactions should be carried out in 20 µl reaction volume containing approximately 20 ng of template DNA, 100µm each of dNTPs, 1.25 pmole of each primer, 1.5mM MgCl<sub>2</sub>, 0.5 unit of AmpliTaq Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer (10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed should be: an initial denaturation at 95°C for 10 min, followed by 35 cycles each of denaturation at 95°C for 45 s, annealing at 51°C for 1 min, and extension at 72°C for 2 min. The extension step at 35<sup>th</sup> cycles should be held for 10 min.

**Example 4:**

Establishing the universal nature of our primer and experimental evidences to demonstrate the universal nature of primers:

The universal nature of the primers 'mcb398' and 'mcb 869' was ensured by the following measures:

(a) Selecting the primers from the aligned cytochrome b gene sequences of 221 animal of distantly related species:

The cytochrome b gene sequences (1140 bp) were aligned using software *CLUSTAL X* (1.8). The region of cytochrome b gene that was most conserved amongst 221 animal species was selected to design the primers.

(b) Selecting the 3' and 5' ends of the primers at the highly conserved positions of cytochrome b gene:

The 3' and 5' ends of the primers were ensured to anneal to a highly conserved position amongst 221 animal species representing a vast range of animal families. It was done to ensure an efficient amplification of all the species in PCR. These positions are shown with star (\*) mark in Table 2.

(c) Ensuring either 'G' or 'C' at the 3' end of the primers:

It was ensured the primers to have either 'G' or 'C' at its 3' ends as these are the nucleotides that ensure the strong bonding at the 3' ends of the primers due to three hydrogen bonds while pairing with each other. The strong bonding at 3' ends helps the primers to anneal properly with its template resulting in significant amplification in PCR.

(d) Selecting the sequences of the primers to ensure a higher internal stability, higher P, S score, and no primer dimer and loop formation:

The sequences of the primers were selected to have a high P, S score for a vast range of animal species (Shown in Table 1). The care was taken to exclude the possibilities of loop or primer dimer formation that could reduce the efficiency of the primers in PCR.

(e) Selecting the sequence of the primers with a comparable melting temperature:

The sequences of the primers were selected to have a comparable melting temperature so that these could work together to amplify a DNA template in PCR at a similar annealing temperature. The melting temperature of both the primers was about 58 degree centigrade and the annealing temperature used in PCR is 51 degree centigrade.

Experimental evidences to demonstrate the universal nature of primers:

(1) Evidence from *In-silico* analysis :

(a) Selecting the primers within the most conserved region of mitochondrial cytochrome b gene

As mentioned above, the primers were designed to anneal within a highly conserved region of mitochondrial cytochrome b gene fragment of 472 bp. Table 2 presents the alignment of the above fragment of cytochrome b gene of 221 animal species representing a vast range of animal families. The conserved positions of nucleotide sequences are shown with star (\*) mark in Table 2

Table 2 also demonstrates that the 3' ends of the primers are highly conserved amongst all the animal species analyzed *in-silico*. In the aligned sequences, the conserved nucleotides are marked with symbol (\*). Also, the 5' end of the primers were selected within the conserved region of cytochrome b gene to improve the probability and stability of match of the primers to their target sequences (i.e. the above mentioned 472 bp fragment of cytochrome b gene). The primers were thoroughly checked for internal stabilities, loop or dimmer formation using different software viz., 'Amplify (1.2)', 'Primer3' (<http://www.genome.wi.mit.edu/cgi-bin/primer/primer3.cgi>) as well as manually.

(b) P, S, score analysis:

We assigned the P,S score (P=Probability of match, S=Stability of match) to the primers for each template using the software *Amplify (1.2)*. The higher scores of P and S ensure a good amplification if all other conditions standard (which are mentioned under 'Example 3') are optimum. The Highest score for 'mcb398' was 98,63 (i.e. the situation where the primer has perfect match with template); however, the highest P, S for 'mcb869' was recorded as 98, 68 for a complete match between the primer and template. The lowest P,S score observed for 'mcb398' was 81,50 for species *Talpa europaea* whereas 'mcb869' had a high P, S score for this species (92, 57). The another species which have lowest P, S score for one of the two primers were *Eumeces egregius* and *Equus ainus*. *Eumeces egregius* had P, S score 86, 55 and 73,51 for 'mcb398' and 'mcb869', respectively; however, the P, S score of *Equus ainus* was calculated as 91,61 and 73, 51 for 'mcb398' and 'mcb869', respectively. All other animals had higher P, S scores then the above mentioned species. To ensure that these primers would work efficiently with the DNA template from the animals having the lowest P, S score for one of the primers, we designed an another experiment to validate the lower limits of one of the two primers sufficient for efficient amplification in PCR. We designed an another primer pair (AFF= 5'ctagtagaatgaatctgaggagg<sup>3'</sup> and AFR= 5'tatgcaaataggaagtatcattc<sup>3'</sup>.) that have more mis-pairing at their annealing sites (but not at ends), therefore have less internal stability

and lower P, S scores for its templates (listed in Table 9). The P,S scores of 'AFF' and 'AFR' were as calculated as low as 41 and 49 for *Platanista gangetica* and *Sus scrofa*. These species were amplified efficiently using the primers 'AFF' and 'AFR' (results shown in Figure 3) (keeping all other conditions standard i.e. the conditions mentioned in 'Example 3'). The lowest P,S scores (86, 55 and 73,51 for species *Eumeces egregius*) for our primers 'mcb398' and 'mcb869', respectively, were higher than the above range of combined P, S scores of 'AFF' and 'AFR' for species *Sus scrofa* (87, 52 and 87, 41), which was efficiently amplified by the primers 'AFF' and 'AFR'. It gives an indication that the primers 'mcb 398' and 'mcb 869' would work with all the species including *Eumeces egregius* efficiently to give rise to the expected product in PCR. This experiment confirmed that the primers 'mcb398' and 'mcb 869' are capable of amplifying the cytochrome b fragment of most of the animal species in a universal manner.

#### © BLAST analysis:

The sequences of primers 'mcb398' and 'mcb869' were blasted against mito and nr databases of NCBI to see its significant alignments with the sequences registered in GenBank. As expected, the most significant alignments of the sequences were found with the cytochrome b gene regions (within the 472 bp fragment mentioned in 'Example 1') of different animal species. This analysis also showed that the 3' as well as 5' ends of the primers were highly conserved amongst a vast range of animal species, confirming the universal nature of the primers (Tables 10 and 11, respectively)

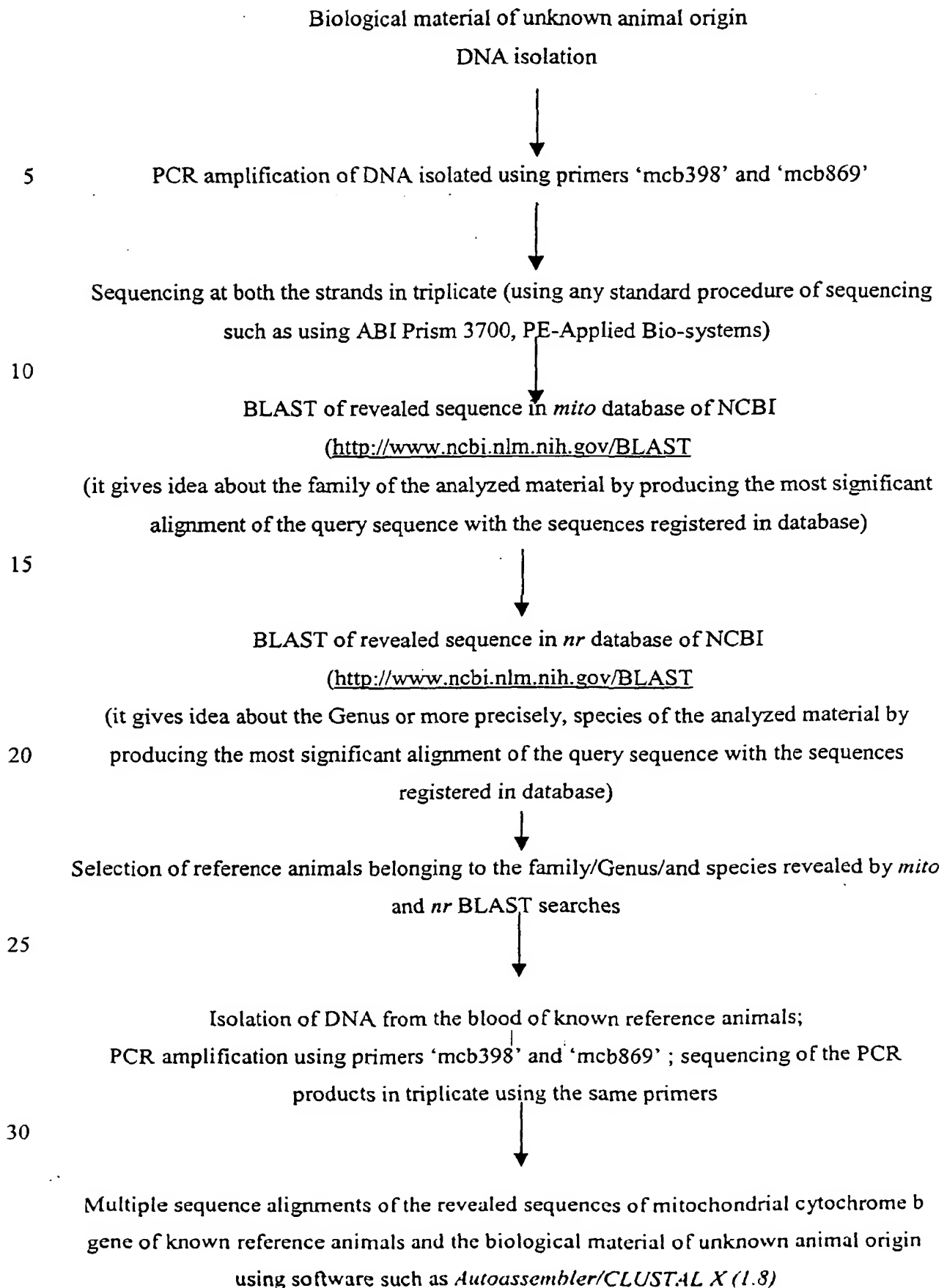
#### (2) Evidence from bench work/experiments done in laboratory conditions:

The DNA from different animals belonging to distantly related species (mentioned in Table 12) was isolated and subjected to PCR amplification using the primers invented by us i.e. the primers 'mcb398' and 'mcb869'. The PCR products amplified were resolved in agarose gel by electrophoresis and visualized under UV light. The PCR products of expected size (472bp) were obtained from all the animals confirming the universal nature of our primers. These results are shown in Figure 4.

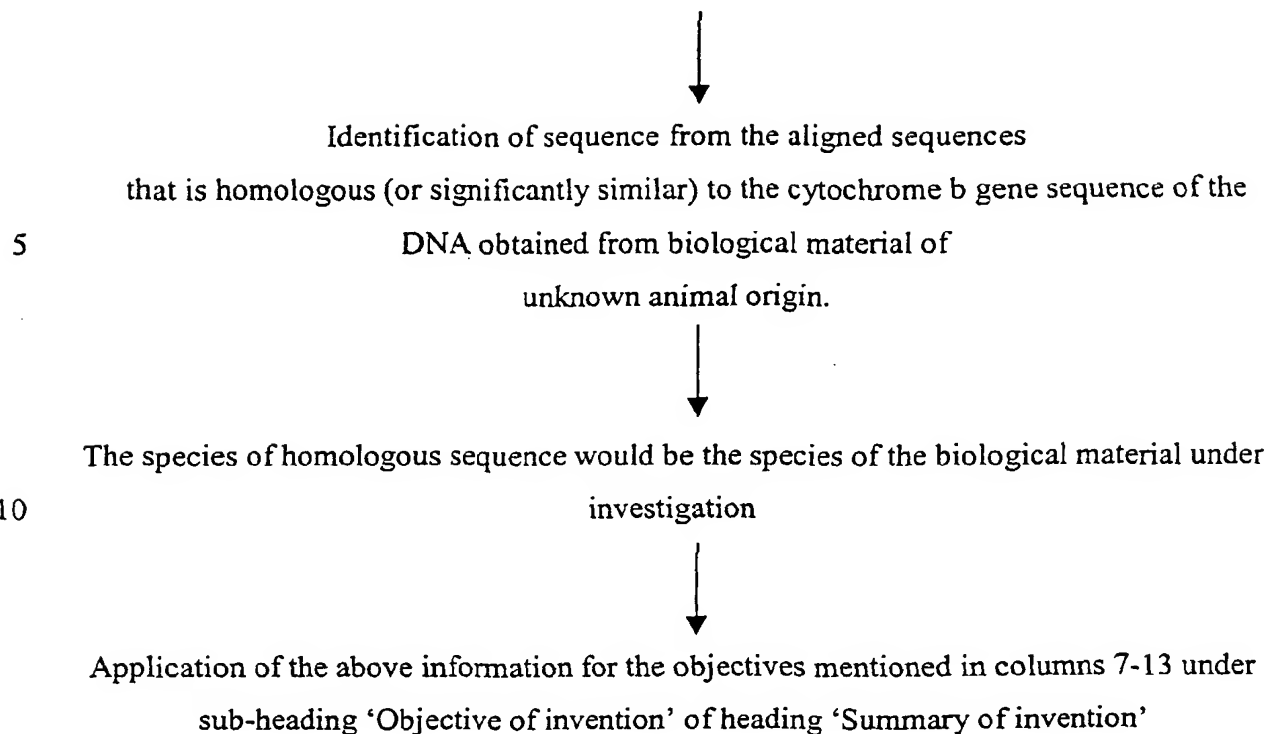
#### Example 5:

Example to establish the identity of confiscated remains from unknown animal origin using the universal primers 'mcb398' and 'mcb869'.

The step-wise procedure to establish the identity of the biological material from an unknown animal source is mentioned below:





**Example 6:**

The actual execution of the technique invented

As a first application and to demonstrate the ease and utility of this method, we investigated a case of forensic identification submitted at our laboratory to seek scientific opinion on animal hunting evidence. In this case, we received the half burned remains of an unknown animal, confiscated by the crime investigation agencies. The DNA was isolated from the above material following standard methods<sup>74</sup> and subjected to PCR amplification using the primers mentioned above (viz., 'mcb398' and 'mcb869'). Amplification reactions were carried out in 20 µl reaction volume containing 20 ng of template DNA, 100µm each of dNTPs, 1.25 pmole of each primer, 1.5mM MgCl<sub>2</sub>, 0.5 unit of AmpliTaq Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer (10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed were: an initial denaturation at 95°C for 10 min, followed by 35 cycles each of denaturation at 95°C for 45 s, annealing at 51°C for 1 min, and extension at 72°C for 2 min. The extension step at 35<sup>th</sup> cycles was held for 10 min.

The PCR products obtained were sequenced in automated work station (ABI Prism 3700, PE-Biosystems) on both strands in triplicate and the sequence resolved (328 bp, shown in Figure 1a) was blasted against *mito* databases of NCBI using BLAST program<sup>73</sup>. The most significant alignment (bits Value 365, E value  $e^{-101}$ ) of this sequence was produced with the cytochrome b gene sequence of *Felis catus*, (Table 3) indicating that species of

analyzed material belongs to family felidae. Further, the above sequence revealed from the confiscated remain was blasted against *nr* databases of NCBI using BLAST program. The most significant alignment (bits Value 603, E value  $e^{-170}$ ) of this sequence was produced with the cytochrome b gene sequence of *Panthera pardus* (Table 4), indicating the identity of the analyzed material as that of a *Panthera pardus* source. Based on this information, we selected the reference animals listed in Table 5 representing different species and subspecies of felidae. The DNA isolated from reference animals was amplified and sequenced on both strands in triplicate using the primer pair mentioned above. Consensus sequences obtained were aligned using program *CLUSTAL X (1.8)* (Table 6). Sequence comparisons identified 113 variable sites in total amongst all animals analyzed (Table 7). Pair-wise comparisons of sequences were performed to find out the variation among different animals investigated. All the species investigated were differentiated by a their unique nucleotides sequences. The molecular signatures of different reference animals were compared with the molecular signature of the confiscated skin 'adil.flesh'. Table 7 demonstrate that the maximum similarity of the adil.flesh with 'gz11' i.e. known Leopard (*Panthera pardus*) species, indicating the identity of the adil.flesh, the confiscated skin, as that of a *Panthera pardus* origin. We also calculated the similarity matrix showing the pair-wise similarity amongst the animal species under investigation using *PHYLIP* software. This matrix is shown in Table 8. It demonstrates that the animals belonging to different species had more variation; however, the animals of same species had maximum similarity among their cytochrome b sequences. The cytochrome b gene sequence of DNA isolated from confiscated material had maximum similarity with the sequences obtained from known Leopard source (99.7%, and 98.2 with 'gz11' and 'gz21', respectively); establishing the identity of the source of confiscated material as that of a Normal leopard (*Panthera pardus*) species. The step-wise procedure involved in above analysis is illustrated in Figure 1a, 1b and 1c, respectively.

Thus, the primers invented by us can generate the molecular signature from any biological material of unknown animal origin, which actually is the characteristic of its family, genus and more precisely, the species. When these signatures are compared *in-silico* with the signatures already available in public databases (viz., GenBank, NCBI database etc) using *BLAST* software<sup>73</sup>, it indicates identity of the family, genus or species of the analyzed material, which in turn is confirmed practically by comparing with the reference animals of the revealed family, genus or species, by including them in the further analysis by the primers 'mcb398' and 'mcb869'. Application of the information revealed could be in

fulfilling the requirements of objectives mentioned in columns 7-13 under sub-heading 'Objective of invention' of heading 'Summary of invention'

The method of the invention can be used to establish the identity of confiscated animal parts and products is one of the key requirements of wildlife identification in forensics. It

5 is needed to establish the crime with the criminal beyond a reasonable doubt to avoid the human violation of wildlife resources. Various morphological biochemical and molecular approaches have been given for this purpose; however, none of the current methods is universally applicable to detect the mutilated animal remains of unknown origin. We have

identified a fragment on the mitochondrial cytochrome b gene, which has enormous  
10 information to differentiate among various animal species back to the family, genus and species sources. We have also found that this fragment is flanked by the highly conserved sequences amongst a vast range of animal species. We invented a pair of universal primer

that can amplify this fragment of DNA isolated from the biological material of an unknown animal origin in polymerase chain reaction (PCR) to reveal its identity at species  
15 and sub-species sources. This novel invention has great potential to revolutionize the whole scenario of wildlife forensic identification and crime investigation.

Table 1. The animal species included in the study for *in-silico* analysis

SN. Code	Name	NCBI accession #	*P,S/F	*P,S/R
1 aep.mel	<i>Aepyceros melampus</i>	AF036289 <sup>1</sup>	97, 60	94, 62
2 ore.ore	<i>Oreotragus oreotragus</i>	AF036288 <sup>1</sup>	88, 52	94, 62
3 add.nas	<i>Addax nasomaculatus</i>	AF034722 <sup>2</sup>	97, 60	95, 66
4 ory.dam	<i>Oryx damah</i>	AJ222685 <sup>1</sup>	90, 58	95, 66
5 hip.equ	<i>Hippotragus equinus</i>	AF022060 <sup>3</sup>	98, 63	85, 55
6 alc.bus	<i>Alcelaphus buselaphus</i>	AJ222681 <sup>1</sup>	97, 60	98, 68
7 sig.lic	<i>Sigmoceros lichtensteinii</i>	AF034967 <sup>4</sup>	97, 60	98, 68
8 bea.hun	<i>Beatragus hunteri</i>	AF034968 <sup>4</sup>	97, 60	94, 62
9 dam.lun	<i>Damaliscus lunatus</i>	AF016635 <sup>3</sup>	97, 60	77, 55
10 con.tau	<i>Connochaetes taurinus</i>	AF016638 <sup>3</sup>	82, 56	93, 62
11 bis.bon	<i>Bison bonasus</i>	Y15005 <sup>5</sup>	90, 58	87, 63
12 bos.gru	<i>Bos grunniens</i> *	AF091631 <sup>6</sup>	90, 58	94, 62
13 bos.tra	<i>Bos tragocamelus</i> *	AJ222679 <sup>1</sup>	90, 58	95, 66
14 buba.bub	<i>Bubalus bubalis</i> *	D34637 <sup>7</sup>	97, 60	93, 64
15 bub.min	<i>Bubalus mindorensis</i>	D82895 <sup>8</sup>	97, 60	87, 62
16 tra.ang	<i>Tragelaphus angasii</i>	AF091633 <sup>6</sup>	97, 60	87, 63
17 tra.eur	<i>Tragelaphus eurycerus</i>	AF036276 <sup>1</sup>	90, 58	97, 64
18 nem.cau	<i>Nemorhaedus caudatus</i> *	U17861 <sup>9</sup>	95, 61	93, 59
19 pse.nay	<i>Pseudois nayaaur</i>	AF034732 <sup>2</sup>	89, 55	89, 59
20 amm.ler	<i>Ammotragus lervia</i>	AF034731 <sup>2</sup>	94, 58	97, 63
21 cap.fal	<i>Capra falconeri</i> *	D84202 <sup>10</sup>	98, 63	95, 66
22 cap.ibe	<i>Capra ibex</i> *	AF034735 <sup>2</sup>	98, 63	89, 58
23 hem.jem	<i>Hemitragus jemlahicus</i> *	AF034733 <sup>2</sup>	95, 61	90, 61
24 rup.pyr	<i>Rupicapra pyrenaica</i>	AF034726 <sup>2</sup>	95, 61	89, 59
25 rup.rup	<i>Rupicapra rupicapra</i>	AF034725 <sup>2</sup>	95, 61	94, 64
26 pan.hod	<i>Pantholops hodgsoni</i>	AF034724 <sup>2</sup>	98, 63	95, 66
27 bud.tax.tax	<i>Budorcas taxicolor taxicolor</i> *	U17868 <sup>9</sup>	90, 53	95, 66
28 ovi.amm	<i>Ovis ammon</i> *	AF034727 <sup>2</sup>	98, 63	97, 64
29 ovi.vig	<i>Ovis vignei</i> *	AF034729 <sup>2</sup>	98, 63	97, 64
30 cap.cri	<i>Capicornis crispus</i> *	AJ304502 <sup>11</sup>	98, 63	94, 63
31 ovi.mos	<i>Ovibos moschatus</i>	U17862 <sup>9</sup>	98, 63	92, 61
32 ore.ame	<i>Oreamnos americanus</i>	AF190632 <sup>12</sup>	98, 63	94, 62
33 cep.dor	<i>Cephalophus dorsalis</i>	AF091634 <sup>6</sup>	97, 58	90, 61
34 cep.max	<i>Cephalophus maxwellii</i>	AF096629 <sup>13</sup>	97, 60	88, 53
35 alc.alc	<i>Alces alces</i>	AJ000026 <sup>14</sup>	95, 61	93, 59
36 hyd.ine	<i>Hydropotes inermis</i>	AJ000028 <sup>14</sup>	97, 60	90, 63
37 mun.mun	<i>Muntiacus muntjak</i> *	AF042718 <sup>15</sup>	90, 58	93, 64
38 cer.ele.kan	<i>Cervus elaphus kansuensis</i> *	AB021098 <sup>16</sup>	98, 63	82, 59
39 cer.ele.xan	<i>Cervus elaphus xanthopygus</i> *	AB021097 <sup>16</sup>	98, 63	82, 59
40 cer.ele.can	<i>Cervus elaphus canadensis</i> *	AB021096 <sup>16</sup>	98, 63	90, 61
41 cer.nip.ce	<i>Cervus nippon centralis</i>	AB021094 <sup>16</sup>	98, 63	90, 61
42 cer.nip.ye	<i>Cervus nippon yesoensis</i>	AB021095 <sup>16</sup>	98, 63	90, 61
43 cer.nip.ke	<i>Cervus nippon keramuc</i>	AB021091 <sup>16</sup>	98, 63	90, 61

44	cer.nip.pu	<i>Cervus nippon pulchellus</i>	AB021090 <sup>16</sup>	98, 63	90, 61
45	cer.nip.ni	<i>Cervus nippon nippon</i>	AB021093 <sup>16</sup>	98, 63	90, 61
46	cer.ela.sc	<i>Cervus elaphus scoticus</i>	AB021099 <sup>16</sup>	98, 63	90, 61
47	cer.dam	<i>Cervus dama</i>	AJ000022 <sup>14</sup>	98, 63	88, 53
48	ran.tar	<i>Rangifer tarandus</i>	AJ000029 <sup>14</sup>	98, 63	89, 57
49	mos.fus	<i>Moschus fuscus</i> *	AF026838 <sup>17</sup>	90, 59	90, 61
50	mos.leu	<i>Moschus leucogaster</i> *	AF026839 <sup>17</sup>	90, 59	90, 61
51	mos.chr	<i>Moschus chrysogaster</i> *	AF026837 <sup>17</sup>	90, 59	90, 61
52	mos.ber	<i>Moschus berezovskii</i> *	AF026836 <sup>17</sup>	90, 59	90, 61
53	mos.mos	<i>Moschus moschiferus</i> *	AF026833 <sup>17</sup>	90, 59	92, 61
54	kob.ell	<i>Kobus ellipsiprymnus</i>	AF022059 <sup>3</sup>	91, 61	95, 66
55	kob.meg	<i>Kobus megaceros</i>	AJ222686 <sup>1</sup>	91, 61	83, 56
56	red.aru	<i>Redunca arundinum</i>	AF096623 <sup>13</sup>	91, 61	94, 62
57	red.ful	<i>Redunca fulvorufula</i>	AF036284 <sup>1</sup>	89, 57	94, 62
58	neo.mos	<i>Neotragus moschatus</i>	AJ222683 <sup>1</sup>	89, 57	94, 62
59	pel.cap	<i>Pelea capreolus</i>	AF022055 <sup>3</sup>	91, 61	90, 61
60	ant.cer	<i>Antilope cervicapra</i> *	AF022058 <sup>3</sup>	82, 56	93, 64
61	sai.tat	<i>Saiga tatarica</i>	AF064487 <sup>18</sup>	91, 61	92, 61
62	gaz.dam	<i>Gazella dama</i>	AF025954 <sup>3</sup>	91, 61	92, 61
63	our.our	<i>Ourebia ourebi</i>	AF036288 <sup>1</sup>	82, 56	82, 59
64	gaz.gaz	<i>Gazella gazella</i> *	AJ222682 <sup>1</sup>	91, 61	89, 57
65	rap.mel	<i>Raphicerus melanotis</i>	AF022053 <sup>3</sup>	81, 54	80, 50
66	mad.kir	<i>Madoqua kirkii</i>	AF022070 <sup>3</sup>	90, 58	97, 65
67	ant.lame	<i>Antilocapra americana</i>	AF091629 <sup>6</sup>	98, 63	98, 68
68	tra.jav	<i>Tragulus javanicus</i> *	D32189 <sup>19</sup>	86, 57	86, 59
69	tra.nap	<i>Tragulus napu</i> *	X56288 <sup>20</sup>	81, 52	93, 58
70	bal.acu	<i>Balaenoptera acutorostrata</i>	X75753 <sup>21</sup>	89, 56	97, 61
71	bal.bon	<i>Balaenoptera bonaerensis</i>	X75581 <sup>21</sup>	89, 56	93, 59
72	bal.bor	<i>Balaenoptera borealis</i> *	X75582 <sup>21</sup>	89, 56	93, 59
73	bal.edi	<i>Balaenoptera edeni</i>	X75583 <sup>21</sup>	89, 56	88, 54
74	esc.rob	<i>Eschrichtius robustus</i> *	X75585 <sup>21</sup>	97, 61	86, 57
75	bal.mus	<i>Balaenoptera musculus</i> *	NC_001601 <sup>22</sup>	97, 57	93, 59
76	meg.nov	<i>Megaptera novaeangliae</i> *	X75584 <sup>21</sup>	97, 61	94, 63
77	bal.phy	<i>Balaenoptera physalus</i> *	NC_001321 <sup>23</sup>	97, 57	94, 63
78	cap.mar	<i>Caperea marginata</i>	X75586 <sup>21</sup>	93, 55	91, 53
79	cep.com	<i>Cephalorhynchus commersonii</i>	AF084073 <sup>24</sup>	85, 51	88, 55
80	cep.eut	<i>Cephalorhynchus eutropia</i> *	AF084072 <sup>24</sup>	85, 51	92, 59
81	lag.obl	<i>Lagenorhynchus obliquidens</i>	AF084067 <sup>24</sup>	94, 59	92, 59
82	cep.heu	<i>Cephalorhynchus heavisidii</i>	AF084070 <sup>24</sup>	89, 56	97, 63
83	cep.hec	<i>Cephalorhynchus hectori</i> *	AF084071 <sup>24</sup>	89, 56	92, 59
84	lag.aus	<i>Lagenorhynchus australis</i>	AF084069 <sup>24</sup>	86, 54	92, 59
85	lag.cru	<i>Lagenorhynchus cruciger</i>	AF084068 <sup>24</sup>	86, 54	92, 59
86	lag.obs	<i>Lagenorhynchus obscurus</i>	AF084066 <sup>24</sup>	86, 54	92, 59
87	lis.bor	<i>Lissodelphis borealis</i>	AF084064 <sup>24</sup>	85, 51	92, 59
88	lis.per	<i>Lissodelphis peronii</i>	AF084065 <sup>24</sup>	86, 54	92, 59
89	glo.mac	<i>Globicephala macrorhynchus</i>	AF084055 <sup>24</sup>	94, 59	88, 55
90	glo.mel	<i>Globicephala melas</i>	AF084056 <sup>24</sup>	94, 59	88, 55
91	fer.att	<i>Feresa attenuata</i> *	AF084052 <sup>24</sup>	94, 59	92, 59

92	pep.ele	<i>Peponocephala electra</i> *	AF084053 <sup>24</sup>	94, 59	88, 55
93	gra.gri	<i>Grampus griseus</i>	AF084059 <sup>24</sup>	97, 61	89, 59
94	pse.cra	<i>Pseudorca crassidens</i> *	AF084057 <sup>24</sup>	94, 59	92, 59
95	lag.acu	<i>Lagenorhynchus acutus</i>	AF084075 <sup>24</sup>	98, 63	89, 59
96	orci.bre	<i>Orcinus orca</i>	AF084061 <sup>24</sup>	86, 57	82, 52
97	orca.bre	<i>Orcaella brevirostris</i>	AF084063 <sup>24</sup>	86, 57	91, 54
98	del.cap	<i>Delphinus capensis</i>	AF084087 <sup>24</sup>	96, 54	97, 63
99	del.tro	<i>Delphinus tropicalis</i>	AF084088 <sup>24</sup>	97, 57	97, 63
100	del.del	<i>Delphinus delphis</i>	AF084085 <sup>24</sup>	97, 57	97, 63
101	sten.cly	<i>Stenella clymene</i>	AF084083 <sup>24</sup>	97, 57	97, 63
102	sten.coe	<i>Stenella coeruleoalba</i>	AF084082 <sup>24</sup>	97, 57	97, 66
103	tur.adu	<i>Tursiops aduncus</i>	AF084092 <sup>24</sup>	97, 57	97, 63
104	sten.fro	<i>Stenella frontalis</i>	AF084090 <sup>24</sup>	97, 57	97, 63
105	saus.chi	<i>Sousa chinensis</i>	AF084080 <sup>24</sup>	97, 57	88, 59
106	sten.lon	<i>Stenella longirostris</i>	AF084103 <sup>24</sup>	97, 61	97, 63
107	turs.tru	<i>Tursiops truncatus</i>	AF084095 <sup>24</sup>	97, 57	96, 59
108	lage.alb	<i>Lagenorhynchus alborostris</i>	AF084074 <sup>24</sup>	97, 61	97, 66
109	sten.bre	<i>Steno bredanensis</i>	AF084077 <sup>24</sup>	97, 61	94, 64
110	sota.flu	<i>Sotalia fluviatilis</i>	AF304067 <sup>25</sup>	97, 61	97, 63
111	del.leu	<i>Delphinapterus leucas</i>	U72037 <sup>26</sup>	97, 61	95, 66
112	mono.mon	<i>Monodon monoceros</i>	U72038 <sup>26</sup>	97, 61	95, 66
113	plat.gan	<i>Platanista gangetica</i> *	AF304070 <sup>25</sup>	97, 61	86, 59
114	plat.min	<i>Platanista minor</i> *	X92543 <sup>27</sup>	97, 61	86, 59
115	kogi.bre	<i>Kogia breviceps</i>	U72040 <sup>26</sup>	97, 59	90, 63
116	kogi.sim	<i>Kogia simus</i>	AF304072 <sup>25</sup>	96, 55	92, 63
117	phys.cat	<i>Physeter catodon</i>	AF304073 <sup>25</sup>	97, 57	80, 58
118	lipo.vex	<i>Lipotes vexillifer</i> *	AF304071 <sup>25</sup>	89, 56	88, 53
119	phoc.sin	<i>phocoena sinus</i>	AF084051 <sup>24</sup>	87, 49	92, 62
120	bera.bai	<i>Berardius bairdii</i>	X92541 <sup>27</sup>	96, 55	90, 59
121	ziph.car	<i>Ziphius cavirostris</i>	X92540 <sup>27</sup>	97, 61	89, 57
122	meso.eur	<i>Mesoplodon europaeus</i>	X92537 <sup>27</sup>	97, 57	90, 61
123	meso.bid	<i>Mesoplodon bidens</i>	X92538 <sup>27</sup>	97, 61	92, 61
124	meso.den	<i>Mesoplodon densirostris</i>	X92536 <sup>27</sup>	91, 61	94, 63
125	hype.amp	<i>Hyperoodon ampullatus</i> *	X92539 <sup>27</sup>	97, 61	90, 65
126	meso.per	<i>Mesoplodon peruvianus</i>	AF304074 <sup>25</sup>	97, 61	86, 58
127	pont.bla	<i>Pontoporia blainvillei</i>	AF304069 <sup>25</sup>	92, 59	88, 55
128	hipp.amp	<i>Hippopotamus amphibius</i>	Y08813 <sup>29</sup>	92, 58	95, 66
129	hex.lib	<i>Hexaprotodon liberiensis</i>	Y08814 <sup>29</sup>	98, 63	97, 66
130	rhin.son	<i>Rhinoceros sondaicus</i> *	AJ245723 <sup>10</sup>	90, 59	87, 61
131	cera	<i>Ceratotherium simum</i>	NC_001808 <sup>12</sup>	90, 59	90, 63
132	dic.sum	<i>Dicerorhinus sumatrensis</i>	AJ245723 <sup>10</sup>	90, 59	86, 57
133	equu	<i>Equus asinus</i>	NC_001755 <sup>11</sup>	91, 61	73, 51
134	baby.bab	<i>Babyrousa babyrussa</i>	Z50106 <sup>11</sup>	89, 56	85, 56
135	phac.afr	<i>Phacochoerus africanus</i>	Z50090 <sup>11</sup>	90, 59	87, 54
136	sus.scr.ew	<i>Sus scrofa haplotype EWBJ</i> *	AF136549 <sup>14</sup>	97, 57	83, 54
137	sus.bar	<i>Sus barbatus</i>	Z50107 <sup>11</sup>	97, 57	85, 55
138	lama.gla	<i>Lama glama</i>	U06429 <sup>11</sup>	89, 55	85, 53
139	lama.gua	<i>Lama guanicoe</i>	Y08812 <sup>29</sup>	88, 54	86, 57

140 vic.vic	<i>Vicugna vicugna</i>	U06430 <sup>35</sup>	89, 55	85, 53
141 cam.bac	<i>Camelus bactrianus</i>	U06427 <sup>35</sup>	94, 58	86, 58
142 arc.for	<i>Arctocephalus forsteri</i>	X82293 <sup>36</sup>	97, 60	87, 64
143 arc.gaz	<i>Arctocephalus gazella</i>	X82292 <sup>36</sup>	94, 58	87, 64
144 eum.jub	<i>Eumetopias jubatus</i>	X82311 <sup>36</sup>	97, 57	86, 57
145 zal.cal	<i>Zalophus californianus</i>	X82310 <sup>36</sup>	89, 55	86, 57
146 odo.ros	<i>Odobenus rosmarus</i>	X82299 <sup>36</sup>	91, 61	81, 52
147 pho.vit	<i>Phoca vitulina</i>	X82306 <sup>36</sup>	90, 58	87, 64
148 pho.fascia	<i>Phoca fasciata</i>	X82302 <sup>36</sup>	98, 63	95, 66
149 pho.gro	<i>Phoca groenlandica</i>	X82303 <sup>36</sup>	92, 59	90, 61
150 cys.cri	<i>Cystophora cristata</i>	X82294 <sup>36</sup>	89, 56	87, 64
151 hyd.lep	<i>Hydrurga leptonyx</i>	X82297 <sup>36</sup>	89, 55	82, 54
152 lep.wed	<i>Leptonychotes weddelli</i>	X72005 <sup>37</sup>	98, 63	91, 66
153 mir.leo	<i>Mirounga leonina</i>	X82298 <sup>36</sup>	89, 55	82, 59
154 eri.bar	<i>Erignathus barbatus</i>	X82295 <sup>36</sup>	89, 56	87, 63
155 mon.sch	<i>Monachus schauinslandi</i>	X72209 <sup>37</sup>	91, 61	87, 60
156 hela.mal	<i>Helarctos malayanus</i> *	U18899 <sup>38</sup>	84, 54	90, 63
157 sel.thi	<i>Selenarctos thibetanus</i> *	AB020910 <sup>39</sup>	89, 57	87, 64
158 ail.ful	<i>Ailurus fulgens</i> *	X94919 <sup>40</sup>	93, 55	87, 64
159 fel	<i>Felis catus</i>	NC_001700 <sup>41</sup>	85, 56	90, 63
160 can	<i>Canis familiaris</i>	NC_002008 <sup>42</sup>	98, 58	84, 54
161 tal	<i>Talpa europaea</i>	NC_002391 <sup>43</sup>	81, 50	92, 57
162 gla.sab	<i>Glaucornys sabrinus</i>	AF011738 <sup>44</sup>	90, 59	82, 54
163 gla.vol	<i>Glaucornys volans</i>	AB030261 <sup>45</sup>	90, 59	87, 60
164 hyl.pha	<i>Hylomys phayrei</i> *	AB030259 <sup>45</sup>	91, 61	81, 50
165 pet.set	<i>Petinomys setosus</i> *	AB030260 <sup>45</sup>	91, 61	81, 50
166 bel.pea	<i>Belomys pearsonii</i> *	AB030262 <sup>45</sup>	91, 61	87, 64
167 pte.mom	<i>Pteromys momonga</i> *	AB030263 <sup>45</sup>	97, 61	90, 63
168 gala.demi	<i>Galagoides demidoffi</i>	AF271411 <sup>46</sup>	97, 58	87, 64
169 pero.pot	<i>Perodicticus potto</i>	AF271413 <sup>46</sup>	97, 60	87, 63
170 gala.mat	<i>Galago matschiei</i>	AF271409 <sup>46</sup>	97, 60	90, 61
171 gala.moh	<i>Galago moholi</i>	AF271410 <sup>46</sup>	97, 57	95, 66
172 oto.gar	<i>Otolemur garnettii</i>	AF271412 <sup>46</sup>	92, 58	87, 60
173 lor.tar	<i>Loris tardigradus</i> *	U53581 <sup>47</sup>	97, 60	93, 59
174 nyc.cou	<i>Nycticebus coucang</i> *	U53580 <sup>47</sup>	97, 60	95, 66
175 mus	<i>Mus musculus</i>	NC_001569 <sup>48</sup>	97, 60	86, 59
176 gor	<i>Gorilla gorilla</i>	NC_001645 <sup>49</sup>	89, 57	80, 58
177 homo	<i>Homo sapiens sapiens</i>	NC_001807 <sup>50</sup>	96, 55	84, 64
178 dug.dug	<i>Dugong dugong</i> *	U07564 <sup>51</sup>	97, 60	89, 59
179 ele.max	<i>Elephas maximus</i> *	AB002412 <sup>52</sup>	97, 60	76, 57
180 afr.con	<i>Afropavo congensis</i>	AF013760 <sup>53</sup>	97, 58	87, 63
181 pavo.mut	<i>Pavo muticus</i> *	AF013763 <sup>53</sup>	97, 57	87, 63
182 tra.bly	<i>Tragopan blythii</i> *	AF200722 <sup>54</sup>	89, 55	85, 57
183 tra.sat	<i>Tragopan satyra</i> *	AF229837 <sup>54</sup>	89, 55	86, 61
184 tra.cob	<i>Tragopan caboti</i>	AF200723 <sup>54</sup>	89, 55	86, 61
185 tra.tem	<i>Tragopan temminckii</i> *	AF023802 <sup>55</sup>	89, 55	81, 56
186 arg.arg	<i>Argusianus argus</i>	AF013761 <sup>53</sup>	89, 55	87, 63
187 cat.wal	<i>Catrecus wallichi</i> *	AF023792 <sup>53</sup>	88, 54	85, 57

188	cro.cro	<i>Crossoptilon crossoptilon</i> *	AF028794 <sup>53</sup>	89, 55	85, 57
189	sym.rec	<i>Syrnaticus reevesi</i> *	AF028801 <sup>53</sup>	89, 55	85, 57
190	bam.tho	<i>Bambusicola thoracica</i> *	AF028790 <sup>53</sup>	80, 48	94, 64
191	fra.fra	<i>Francolinus francolinus</i>	AF013762 <sup>53</sup>	97, 58	86, 61
192	ith.cru	<i>Ithaginis cruentus</i> *	AF068193 <sup>53</sup>	98, 63	85, 57
193	ant.par	<i>Anthropoides paradisea</i>	U27557 <sup>56</sup>	85, 56	82, 58
194	ant.vir	<i>Anthropoides virgo</i>	U27545 <sup>56</sup>	84, 54	82, 52
195	gru.ant.an	<i>Grus antigone antigone</i>	U11060 <sup>57</sup>	90, 53	87, 63
196	gru.ant.gi	<i>Grus antigone gillae</i>	U11064 <sup>57</sup>	90, 53	87, 63
197	gru.any.sh	<i>Grus antigone sharpei</i>	U11061 <sup>57</sup>	90, 53	87, 63
198	gru.leu	<i>Grus leucogeranus</i> *	U27549 <sup>56</sup>	90, 53	87, 63
199	gru.can.pr	<i>Grus canadensis pratensis</i>	U27553 <sup>56</sup>	97, 60	87, 63
200	gru.can.ro	<i>Grus canadensis rowani</i>	U27552 <sup>56</sup>	97, 60	87, 63
201	gru.can.ta	<i>Grus canadensis tabida</i>	U27551 <sup>56</sup>	98, 63	87, 63
202	gru.can.ca	<i>Grus canadensis canadensis</i>	U27554 <sup>56</sup>	97, 61	87, 63
203	gru.ame	<i>Grus americana</i>	U27555 <sup>56</sup>	90, 53	87, 63
204	gru.gru	<i>Grus grus</i>	U27546 <sup>56</sup>	89, 54	87, 63
205	gru.mon	<i>Grus monacha</i> *	U27548 <sup>56</sup>	90, 53	87, 63
206	gru.nig	<i>Grus nigricollis</i> *	U27547 <sup>56</sup>	90, 53	87, 63
207	gru.jap	<i>Grus japonensis</i>	U27550 <sup>56</sup>	81, 54	87, 63
208	cic.boy	<i>Ciconia boyciana</i> *	NC_002196 <sup>58</sup>	94, 58	79, 60
209	rhe.ame	<i>Rhea americana</i>	AF090339 <sup>59</sup>	93, 63	79, 60
210	ant.alb	<i>Anthracoeros albirostris</i> *	U89190 <sup>60</sup>	97, 61	86, 59
211	fal.fam	<i>Falco femoralis</i>	U83310 <sup>61</sup>	97, 61	86, 60
212	fal.ver	<i>Falco verpertinus</i>	U83311 <sup>61</sup>	97, 61	85, 57
213	fal.par	<i>Falco peregrinus</i> *	U83307 <sup>61</sup>	97, 61	84, 52
214	fal.spa	<i>Falco sparverius</i>	U83306 <sup>61</sup>	92, 59	80, 51
215	ayt.ame	<i>Aythya americana</i>	NC_000877 <sup>62</sup>	98, 63	94, 62
216	smi.sha	<i>Smithornis sharpei</i>	NC_000879 <sup>59</sup>	97, 53	90, 61
217	vid.cha	<i>Vidua chalybeata</i>	NC_000830 <sup>59</sup>	97, 60	87, 64
218	chry.pic	<i>Chrysemys picta</i>	NC_002073 <sup>63</sup>	89, 56	86, 57
219	emy.orb.ku	<i>Emys orbicularis</i>	AJ131425 <sup>64</sup>	90, 59	94, 63
220	che.mud	<i>Chelonia mydas</i> *	AB012104 <sup>65</sup>	90, 58	94, 63
221	eum.egr	<i>Eumeces egregius</i>	AB016606 <sup>65</sup>	86, 55	73, 51



Table 2. Multiple sequence alignment of 472 bp fragment of mitochondrial cytochrome b gene of 221 animal species

PRIMER 'mcb193'	TACCATGAGGACAAATATCATTCTG	.. .. .
aep.mel	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACAAATCTCCTCTCAGCAA	60
ore.ore	TTCCCTGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACTAATCTCCTCTCAGCAA	60
add.nas	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
ory.dam	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATCACTAACCTCTCTCAGCAA	60
hip.equ	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
alc.bus	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
sig.lic	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
bea.hun	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
dam.lun	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACTAACCTCTCTCAGCAA	60
con.tau	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
amm.ler	TGCCATGAGGACAGATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
pse.nay	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACTAACCTCTCTCAGCAA	60
cap.ibe	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
hem.jem	TACCATGAGGACAGATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
cap.fal	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAATCTCCTCTCAGCAA	60
rup.pyr	TACCATGAGGACAGATATCATTCTGAGGAGCAACAGTTATTACCAACCTCTCTCAGCGA	60
rup.rup	TACCATGAGGACAGATATCATTCTGAGGAGCAACAGTTATTACCAATCTTCTCTCAGCAA	60
nem.cau	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCTCAGCAA	60
bud.tax.tax	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAACCTCTCTCAGCAA	60
pan.hod	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAACCTCTCTCAGCAA	60
ovi.amm	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAACCTCTCTCAGCAA	60
ovi.vig	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAACCTCTCTCAGCAA	60
cap.cri	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAACCTCTCTCAGCAA	60
ovi.mos	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAATCTCCTTTTCAAGCAA	60
ore.ame	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCTCAGCAA	60
cep.dor	TGCCATGAGGAGCAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCTCAGCAA	60
cep.max	TGCCATGAGGAGCAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCTCAGCAA	60
bis.bon	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCTCAGCAA	60
bos.gru	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAATCTATTATCAGCAA	60
bos.tra	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
bub.min	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
buba.bub	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
tra.ang	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
tra.eur	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
kob.ell	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
kob.meg	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
red.aru	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTTATTACCTAATCTCTCTCAGCAA	60
red.ful	TGCCATGAGGACAAATATCCTTTTGAGGAGCAACAGTTATTACCTAATCTCTCTCAGCAA	60
neo.mos	TGCCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
pel.cap	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
gat.dam	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
our.our	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
ant.gar	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
sal.tat	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
mad.kir	TGCCATGAGGACAAATATCCTTTTGAGGAGCAACAGTTATTACCTAATCTCTCTCAGCAA	60
rap.mel	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
gat.gat	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTTATTACCTAATCTCTCTCAGCAA	60
ant.ame	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTTATTACCTAATCTCTCTCAGCAA	60
hyd.lne	TGCCATGAGGACAAATATCCTTTTGAGGAGCAACAGTTATTACCTAATCTCTCTCAGCAA	60
mun.mun	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTTATTACCTAATCTCTCTCAGCAA	60
alc.ala	TACCATGAGGACAGATATCCTTTTGAGGAGCAACAGTTATTACCTAATCTCTCTCAGCAA	60
cer.ela kun	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTTATTACCTAATCTCTCTCAGCAA	60

cer.ela.xan TACCATGAGGACAAATATCATTCTGAGGAGCAACGGTCATTACCAACCTTCTCTCAGCAA 60  
cer.ela.can TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA 60  
cer.nip.cent TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA 60  
cer.nip.yes TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA 60  
cer.nip.ker TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA 60  
cer.nip.pul TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA 60  
cer.nip.nip TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA 60  
cer.ela.sco TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA 60  
cer.dam TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA 60  
ran.tar TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA 60  
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lage.alb TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA 60  
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sota.flu TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA 60

del.leu	TACCCTGAGGACAAATATCATTCTGAGGGCGCAACCGTCATTACCAATCTCCTATCAGCAA	60
mono.mon	TACCCTGAGGACAAATATCATTCTGAGGTGCAACCGTCATCACCAACCTCCTATCAGCAA	60
plat.gan	TACCCTGAGGACAAATATCATTCTGAGGTGCAACCGTCATCACCAACCTTTTATCAGCAA	60
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kogi.bre	TACCCTGAGGGCCAAATATCATTCTGAGGAGCAACCGTCATCACCAACCTTATATCCGCCAA	60
kogi.sim	TGCCCTGAGGGCCAAATATCATTCTGAGGAGCAACCGTCATCACAAACCTTATATCCGCCAA	60
phys.cat	TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTTATCACAAACCTTCTATCAGCAA	60
lipo.vex	TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACTAATCTTCTATCAGCAA	60
phoc.sin	TGCCCTGAGGGACAAATATCATTCTGAGGTGCTACCGTCATCACAAACCTCTTATCAGCAA	60
bera.bai	TGCCCTGAGGGCAAAATATCATTCTGAGGTGCAACCGTCATCACCAACCTCCTATCCGCTA	60
ziph.car	TACCCTGAGGACAAATATCATTCTGAGGTGCAACCGTCATCACAAACCTCTTATCCGCTA	60
meso.eur	TTCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTTATTACCAACCTCCTATCCGCCA	60
meso.bid	TACCCTGAGGACAAATATCATTCTGAGGCGCAACCTGTTATTACTAACCTCCTATCCGCTA	60
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hype.amp	TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCCGCCA	60
meso.per	TACCTTGAGGACAAATATCATTCTGAGGCGCAACCTGTCATTACTAATCTTTTATCTGCTA	60
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hex.lib	TACCATGAGGACAAATATCATTCTGAGGGGCAACAGTCATCACCAACTTACTATCAGCTA	60
hipp.amp	TGCCATGAGGACAAATGTCATTCTGAGGGGCAACAGTCATTACCAACTTACTGTCAGCTA	60
dic.sum	TACCATGAGGTCAAATATCCTTCTGAGGAGGCCAAGTTATCAGAAATCTCCTCTCAGCCA	60
rhin.son	TACCATGAGGTCAAATATCCTTCTGAGGGGCTACAGTCATTACAAATCTCCTCTCAGCCA	60
cera	TACCATGAGGCGCAAAATATCCTTCTGAGGGGCTACAGTCATCAGAAACCTCCTCTCAGCTA	60
equu	TACCATGAGGACAAATATCCTTCTGAGGAGCAACCGTCATTACAAACCTCCTATCAGCAA	60
baby.bab	TACCTTGAGGACAAATATCATTCTGAGGAGCTACCGTCATTACAAACCTACTATCAGCCA	60
phac.afr	TACCCTGAGGACAAATATCGTTCTGAGGAGGCCACAGTCATCACAAACCTACTATCAGCCA	60
sus.bar	TGCCCTGAGGACAAATATCATTCTGAGGAGCTACCGTCATCACAAATCTACTATCAGCTA	60
sus.scr.ewb3	TGCCCTGAGGACAAATATCATTCTGAGGAGCTACCGTCATCACAAATCTACTATCAGCTA	60
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cam.bac	TCCCATGAGGACAGATATCATTCTGAGGAGCAACAGTAATTACAAACCTACTCTCAGCAA	60
arc.for	TTCCATGAGGACAAATATCATTCTGAGGAGCAACCGTCATTACCAACCTCCTATCAGCAG	60
arc.gaz	TTCCATGAGGACAGATATCATTCTGAGGAGCAACCGTCATTACCAACCTCCTATCAGCAA	60
eum.jub	TTCCGTGAGGACAAATATCATTCTGAGGAGCAACCGTCATTACCAACCTCCTATCAGCTA	60
sal.cal	TTCCATGAGGACAAATATCATTCTGAGGAGCAACCGTCATTACCAACCTCCTATCAGCAG	60
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pho.gro	TACCATGAGGGCCAAATGTCATTCTGAGGAGCAACAGTTATCACTAATCTACTATCAGCAA	60
pho.vit	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCAACTTACTATCAGCAA	60
cys.cri	TACCGTGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCAACTTACTATCAGCAA	60
hyd.lep	TGCCATGAGGACAAATATCATTCTGAGGAGCAACCGTTATTACCAACTTACTATCAGCAA	60
lep.wed	TACCATGAGGACAAATATCATTCTGAGGAGCAACCGTCATTACCAACTTACTATCAGCAA	60
mir.leo	TGCCATGAGGACAAATATCATTCTGAGGAGCAACCGTCATTACCAACCTACTATCAGCAG	60
eri.bar	TACCATGAGGGCCAAATATCATTCTGAGGAGCAACCGTTATCACCAACCTACTATCAGCAA	60
mon.sch	TACCATGAGGACAAATATCCTTCTGAGGGGCGACCGTCATCACCAACCTACTATCAGCAA	60
hela.mal	TACCCTGAGGGCCAAATGTCCTTCTGAGGAGCAACCTGTCATTACCAATCTCCTATCAGCCA	60
sel.thi	TACCCTGAGGGCCAAATATCCTTCTGAGGAGCGACTGTCATTACCAACCTCCTATCAGCCA	60
ail.ful	TGCCCTGAGGACAGATATCATTCTGAGGAGCAACCGTTATCACCAACCTACTATCAGCCA	60
fel	TACCATGAGGGCCAAATGTCCTTCTGAGGAGCAACCGTAATCACTAAGCTCCTGTCAGCAA	60
can	TACCATGAGGACAAATATCATTCTGAGGAGCAACCTGTAATCACTAATCTTCTCTGTCGA	60
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gla.vol	TACCCTGAGGACAAATATCTTTCTGAGGAGCTAATGTCATCACCAACCTTCTCTCAGCTA	60
hyl.pha	TACCATGAGGACAAATATCTTTCTGAGGGGCTACCGTTATTACAAACCTACTATCTGCCA	60
pet.sec	TACCATGAGGACAAATATCTTTCTGAGGGGCTAAGTTATTACAAACCTACTATCTGCCA	60
bel.pea	TACCATGAGGACAAATATCTTTCTGAGGAGCAACCTGTAATCACTAAGCTTCTCTCAGCTA	60
pte.mom	TACCCTGAGGACAAATATCATTCTGAGGGGCGAATCTTATCACTAAGCTTCTCTCAGCTA	60
gala.demi	TTCCATGAGGGCCAAATATCATTCTGAGGTGCTAAGTAATTACTAAGCTTCTCTCAGCTA	60

pero.pot	TCCCATGAGGACAAATATCATTTCTGAGGTTGCCACAGTAATCACAACCTCCTATCAGCAA	60
gala.mat	TCCCATGAGGACAAATATCATTTCTGAGGCGCTACCGTAATCACAATCTCCTCTCGCAA	60
gala.moh	TTCCGTGAGGACAAATATCATTTCTGAGGCGCTACCGTAATCAGTAACCTCCTCTCAGCAA	60
oto.gar	TCCCATGAGGACAAATGTCTATTTCTGAGGCGCAACCGTAATTACAAATCTCCTCTCAGCAA	60
lor.tar	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACAGTAATTACAAACCTACTATCAGCAA	60
nyc.cou	TCCCATGAGGACAAATATCATTTCTGAGGTGCCACCGTCATCACTAACCTACTATCGGCAA	60
mus	TTCCATGAGGACAAATATCATTTCTGAGGTGCCACAGTTATTACAAACCTCCTATCAGGCA	60
gorr	TCCCATGAGGACAAATATCCTTTCTGAGGAGCCACAGTAATCACAACCTTGCTATCGGCAA	60
homo	TCCCGTGAGGACAAATATCATTTCTGAGGGGGCCACAGTAATTACAAACCTTACTATCGGCAA	60
dug.dug	TCCCATGAGGACAAATATCATTTCTGAGGAGCAACCGTTATTACTAACCTCCTCTCAGCTA	60
ele.max	TTCCATGAGGACAAATATCATTTCTGAGGGGGCAACCGTAATTACTAACCTCTTCTCAGCAA	60
afr.con	TCCCATGAGGACAAATATCATTTCTGAGGGGGCAACCTGTCTACAAAACCTATACTCAGCAA	60
pavo.mut	TCCCATGAGGACAAATATCATTTCTGAGGGGGCAACCTGTCTACAAAACCTATACTCAGCAA	60
tra.bly	TCCCATGAGGACAAATATCATTTTGTAGGGGGCTACCGTCATCACAACCTTATTCTCAGCAA	60
tra.sat	TCCCATGAGGACAAATATCATTTTGTAGGGGGCTACCGTCATTACAAATTTATTCTCAGCAA	60
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tra.tem	TCCCATGAGGACAAATATCATTTTGTAGGGGGCTACCGTCATCACAACCTTATTCTCAGCAA	60
arg.arg	TCCCATGAGGACAAATATCATTTTGTAGGGGGCTACCGTCATCACAACCTTATTCTCAGCAA	60
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cro.cro	TCCCATGAGGACAAATATCATTTTGTAGGGGGCTACCGTCATCACAACCTTATTCTCAGCAA	60
sym.ree	TCCCATGAGGACAAATATCATTTTGTAGGGGGCAACCGTCATCACAACCTTATTCTCAGCAA	60
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fra.fra	TCCCATGAGGACAAATATCATTTCTGAGGGGGCTACCGTCATTACCAACCTATTCTCAGCAA	60
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ant.par	TACCATGAGGACAAATGTCTATTTGTAGGGGGCTACAGTCATCACCATCTCTCTCAGCCG	60
ant.vir	TACCATGAGGACAAATGTCTATTTGTAGGGGGCTACAGTTATCACCATCTCTCTCAGCCG	60
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gru.can.tab	TACCATGAGGACAAATATCATTTCTGAGGGGGCTACAGTCATTACCAACCTCTCTCAGCCG	60
gru.can.can	TACCATGAGGACAAATATCATTTTGTAGGGGGCTACAGTTATCACCATCTCTCTCAGCCG	60
gru.ame	TACCATGAGGACAAATGTCTATTTGTAGGGGGCTACAGTTATCACCATCTCTCTCAGCCG	60
gru.gru	TACCATGAGGACAAATATCATTTTGTAGGGGGCTACAGTTATCACCATCTCTCTCAGCCG	60
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rhe.ame	TACCATGAGGACAAATATCATTTCTGAGGAGCCACAGTTATTACCAACCTATTCTCAGCCA	60
ant.alb	TACCATGAGGACAAATATCATTTCTGAGGGGGCAACCGTCATCACCATCTCTCTCAGCCA	60
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fal.ver	TACCCCTGAGGACAAATATCATTTCTGAGGGGGCAACCGTCATCACCATCTCTCTCAGCAA	60
fal.per	TACCCCTGAGGACAAATATCATTTCTGAGGAGCCACAGTCATTACCAACCTATTCTCAGCAA	60
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ayt.ame	TACCATGAGGACAAATATCATTTCTGAGGGGGCAACCGTCATCACCATCTCTCTCAGCTA	60
smi.sha	TCCCATGAGGACAAATATCATTTCTGAGGTGCTACAGTAATCACCATCTCTCTCAGCAA	60
vid.cha	TGCCATGAGGACAAATATCATTTCTGAGGAGCCACAGTAATCACAACCTATTCTCAGCAA	60
chry.pic	TACCATGAGGACAAATATCCTTTCTGAGGTGCCACCGTTATTACTAACCTCCTCTCAGCCA	60
emy.orb.kur	TACCATGAGGACAAATATCCTTTCTGAGGTGCCACCGTTATTACTAACCTCCTCTCAGCCG	60
che.mud	TACCATGAGGACAAATATCATTTTGTAGGGGGCAACCGTCATCACAACCTACTCTCAGCCA	60
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ran. car	TTCCATATAATTGGTACAAATCTAGTCCGAATGAATTTGAGGAGGCTTTCTGTAGATAAAAG	120
mos. fus	TTCCATACATTGGTACTAATCTGGTTGAATGAATTTGAGGAGGCTTTCTCAGTAGACAAAAG	120
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mos. chr	TTCCATACATTGGTACTAATCTGGTTGAATGAATTTGAGGAGGCTTTCTCAGTAGACAAAAG	120
mos. ber	TTCCCTTACATTGGTACTAATCTGGTTGAATGAATTTGAGGAGGCTTTCTCAGTAGACAAAAG	120
mos. mos	TTCCCTTACATTGGTACTAATCTGGTTGAATGAATTTGAGGAGGCTTTCTCAGTAGACAAAAG	120
tra. jav	TCCCATACATTGGCAGACAGCTTGGTGAATGAATCTGAGGCTGGTTTCTCAGTAGACAAAAG	120
trag. nap	TCCCTTATATCGGCACCGAACTAGTTGAATGAATCTGAGGCTGGCTTCTGTGTAGACAAAAG	120
bala. acu	TCCCATACATTGGTACTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGACAAAAG	120
bala. bon	TCCCATACATTGGTACTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
bala. bor	TCCCATACATTGGTACTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
bala. edi	TCCCATACATTGGTACTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
esch. rob	TCCCATACATTGGCCTACTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
bala. mus	TCCCATACATTGGTACTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
mega. nov	TCCCATACATTGGTACTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
bala. phy	TCCCATACATTGGTACTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
cap. mar	TCCCATATATTGGTACCACCTAGTTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
ceph. com	TCCCTTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
ceph. eut	TCCCTTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
lage. obl	TCCCTTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
ceph. hea	TCCCTTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
ceph. hec	TCCCTTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
lage. aus	TCCCTTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
lage. cru	TCCCTTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
lage. obs	TCCCTTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
lisso. bor	TCCCTTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
lisso. per	TCCCTTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
gio. mac	TCCCTTACATCGGCACCTACCTTAGTAGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
gio. mel	TCCCTTACATCGGCACCTACCTTAGTAGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
fer. att	TCCCTTACATCGGCACCTACCTTAGTAGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
pepo. ele	TCCCTTACATCGGCACCTACCTTAGTAGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
gram. gri	TCCCTTACATCGGCACCTACCTTAGTAGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
pse. cra	TCCCTTACATCGGCACCTACCTTAGTAGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
lage. acu	TCCCTTACATCGGCACCTACCTTAGTAGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
orci. bre	TCCCTTACATCGGCACCTACCTTAGTAGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
orca. bre	TCCCTTACATCGGCACCTACCTTAGTAGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
del. cap	TCCCTTATATTGGGCACTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
del. tro	TCCCTTATATTGGGCACTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
del. dal	TCCCTTATATTGGGCACTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
sten. cly	TCCCTTATATTGGGCACTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
sten. coe	TCCCTTATATTGGGCACTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
tur. adu	TCCCTTATATTGGGCACTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
sten. fro	TCCCTTATATTGGGCACTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
saus. chi	TCCCTTACATTGGGCACTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
sten. lon	TCCCTTATATTGGGCACTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
turs. tru	TCCCTTATATTGGGCACTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
lage. alb	TCCCTTATATTGGGCACTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
sten. bre	TCCCTTACATCGGCACCTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
sota. flu	TCCCTTACATCGGCACCTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
del. leu	TCCCTTACATCGGCACCTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
mono. mon	TCCCTTATATTGGGCACTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
plat. gan	TCCCTTATATTGGGCACTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
plat. min	TCCCTTATATTGGGCACTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
kogi. bre	TCCCTTATATTGGGCACTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
kogi. sim	TCCCTTATATTGGGCACTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
phys. sat	TCCCTTATATTGGGCACTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
lipo. wak	TCCCTTACATCGGCACCTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120
phoc. sin	TCCCTTACATCGGCACCTACCTTAGTGAATGAATCTGAGGCTGGCTTCTGTGTAGATAAAAG	120



bera.bai	TTCCCTTATATCGGCACCACTCTTGTGGAATGAATCTGAGGTGGCTTCTCCGTAGATAAAAG	120
ziph.car	TCCCTTATATCGGCACCTACTCTAGTGAATGAATCTGAGGTGGCTTTTTCAGTAGATAAAAG	120
meso.eur	TCCCTTATATTGGCACTACTCTAGTGAATGAATCTGAGGTGGCTTTTTCAGTAGATAAAAG	120
meso.bid	TTCCCTACATCGGCACCTACCCTAGTGAATGAATCTGAGGTGGCTTTTTCAGTAGACAAAAG	120
meso.den	TTCCCTTATATTGGCACCACTAGTGAATGAATCTGAGGTGGCTTTTTCAGTAGACAAAAG	120
hype.amp	TTCCCTTATATCGGCACCTACCCTAGTGAATGAATCTGAGGTGGCTTTTTCAGTAGACAAAAG	120
meso.per	TCCCTTATATTGGCACCACTAGTGAATGAATCTGAGGTGGCTTCTCCGTAGATAAAAG	120
pons.bla	TCCCTTACATCGGAACCTACCCTGTAGAATGAATCTGAGGTGGCTTTTCTGTAGACAAAAG	120
hex.lib	TCCCTTACATTGGGAACAGACCTAGTAGAATGAATCTGAGGAGGCTTTTCTGTAGATAAAAG	120
hipp.amp	TCCCTTATATTGGGAACAGACCTAGTAGAATGAATCTGAGGAGGCTTTTCTGTAGATAAAAG	120
dic.sum	TCCCATACATCGGCACCGACCTTGTAGAATGAATCTGAGGGGGATTCTCCGTAGACAAAAG	120
rhin.son	TCCCTTATATCGGTACCAACCTTGTAGAGTGAATCTGAGGAGGATTCTCAGTCGACAAAAG	120
cera	TCCCTTACATCGGCACCAACCTCGTAGAATGAATCTGAGGAGGATTCTCCGTGACAAAAG	120
equu	TCCCTTACATCGGCACCTACTCGTGAATGAATCTGAGGTGGATTCTCAGTAGACAAAAG	120
baby.bab	TTCCCTTATATCGGAACCGACCTCGTAGAATGAATCTGAGGAGGCTTCTCCGTGACAAAAG	120
phac.afr	TCCCTTACATTGGGAACAAATCTTGTAGAATGAATCTGAGGAGGTTTCTCCGTGACAAAAG	120
sus.bar	TCCCTTATATCGGAACAGACCTCGTAGAATGAATCTGAGGGGGCTTTTCTCCGTGACAAAAG	120
sus.scr.ewb3	TCCCTTATATCGGAACAGACCTCGTAGAATGAATCTGAGGGGGCTTTTCTCCGTGACAAAAG	120
lama.gla	TTCCATATGTTGGCACCACTAGTGAATGAATTTGAGGAGGATTCTCCGTAGACAAAAG	120
lama.gua	TTCCATATGTTGGCACCACTAGTGAATGAATTTGAGGGGGGTTCTCCGTAGATAAAAG	120
vic.vic	TTCCATACGTTGGTACAACACTAGTGAATGAATTTGAGGAGGATTCTCCGTAGATAAAAG	120
cam.bac	TTCCCTTATATCGGCACCACTAGTAGAATGAATTTGAGGTGGCTTCTCCGTAGACAAAAG	120
arc.for	TCCCTTACATTGGGACCAACCTAGTAGAATGAATCTGAGGAGGATTCTCAGTTGATAAAG	120
arc.gaz	TCCCTTACATCGGAACCTAACCTAGTAGAATGAATCTGAGGAGGATTCTCAGTTGATAAAG	120
eum.jub	TCCCTTACATCGGAACCAACCTAGTAGAATGAATCTGAGGGGGATTCTCAGTCGACAAAAG	120
zal.cal	TCCCTTACATCGGAACCAACCTAGTAGAATGAATTTGAGGGGGATTCTCAGTCGACAAAAG	120
odo.ros	TTCCCTATGTTAGGGAGCTGACTTGGTGAATGAGTCTGAGGGGGGTTTTCAGTTGATAAAG	120
pho.fasciata	TTCCCTTATATCGGAACCGACCTAGTAGAATGAATCTGAGGAGGATTCTCAGTTGATAAAG	120
pho.gro	TCCCTTACATCGGAACCGATCTAGTAGAATGAATCTGAGGAGGTTCTCAGTTGATAAAG	120
pho.vit	TCCCTTATGTTGGGAACCGACCTTGTAGAATGAATCTGAGGAGGTTTCTCAGTAGATAAAG	120
cys.cri	TCCCTTACATCGGAGCCGATCTAGTAGAATGAATCTGAGGGGGATTCTCAGTCGATAAAG	120
hyd.lep	TTCCCTTACATCGGAACCGACCTAGTAGAATGAATTTGAGGCGGATTCTCAGTCGACAAAAG	120
lep.wed	TTCCCTTACATCGGAACCTGACTTAGTAGAATGAATCTGAGGCGGATTCTCAGTTGACAAAAG	120
mir.leo	TCCCTTATGTTGGGAGACGACCTAGTAGAATGAATCTGAGGAGGATTCTCAGTTGACAAAAG	120
eri.bar	TCCCTTACATCGGACCTGATCTAGTAGAATGAATCTGAGGAGGATTCTCAGTTGACAAAAG	120
mon.sch	TCCCTTACATCGGAACCGATCTAGTAGAATGAATCTGAGGCGGTTCTCAGTAGATAAAG	120
hela.mal	TCCCTTATATTGGGAACCGACCTAGTAGAATGAATCTGAGGAGGCTTTTCTGTAGACAAAAG	120
sel.thi	TCCCTTATATTGGGAACAGACCTAGTAGAATGAATCTGAGGGGGCTTTTCTGTAGATAAAG	120
ail.ful	TTCCCTTATATTGGGAACCTAACCTTGTAGAGTGAATCTGAGGAGGTTTCTCAGTCGACAAAAG	120
fel	TTCCATACATCGGCACTGAACCTAGTAGAATGAATCTGAGGGGGGTTCTCAGTAGACAAAAG	120
can	TCCCTTATATCGGGAACCTGACTTAGTAGAATGAATCTGAGGCGGCTTCTCAGTTGACAAAAG	120
cal	TTCCCTTACATCGGTACAGACTTAGTAGAATGAATTTGAGGTGGCTTCTCAGTCGACAAAAG	120
gla.sab	TTCCCTTATATTGGGACAACACTTGTAGAATGAATCTGAGGAGGCTTCTCAGTTGATAAAG	120
gla.vol	TTCCCTTATATTGGTACACACTTGTAGAATGAATCTGAGGGGGCTTCTCAGTTGATAAAG	120
hyl.pha	TCCCTTACATTGGGAACCTCTTGTGAATGAATTTGAGGGGGATTCTCCGTAGATAAAG	120
pet.see	TCCCTTATATTGGGAACCTCTTGTGAATGAATTTGAGGGGGATTCTCCGTAGATAAAG	120
bel.pea	TCCCTTATATTGGGAACCTCTTGTGAATGAATTTGAGGGGGATTCTCCGTAGATAAAG	120
pte.mom	TCCCTTATATCGGCACCAACCTTGTGAATGAATCTGAGGGGGATTCTCCGTAGATAAAG	120
gala.demi	TCCCATATATAGGGCCTACTCTAGTAGAATGAATCTGAGGGGGATTCTCCGTAGACAAAAG	120
pero.pot	TCCCATATGTTAGGTAGAACCTTGTAGAATGAATTTGAGGGGGATTCTCAGTAGACAAAAG	120
gala.mat	TTCCCTTACATCGGTACCGGCTAGTAGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG	120
gala.moh	TTCCCTTATATAGGAACCTAGTAGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG	120
oto.gar	TTCCCTTACATAGGAACCTAGTAGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG	120
lps.bar	TTCCCTTACATCGGAACCTAGTAGAATGAATCTGAGGGGGATTCTCAGTAGATAAAG	120
lys.cou	TCCCTTATATTGGGACAACCTAGTAGAATGAATTTGAGGGGGATTCTCAGTAGATAAAG	120
mus	TCCCATATATTGGGAACCAACCTAGTAGAATGAATTTGAGGGGGATTCTCAGTAGATAAAG	120
garc	TCCCTTACATCGGAACAGACCTAGTAGAATGAATTTGAGGGGGATTCTCAGTAGATAAAG	120
homo	TCCCATACATTGGGACCAACCTAGTAGAATGAATTTGAGGGGGATTCTCAGTAGATAAAG	120

dug.dug	TCCCCTACATCGGCAACCAACCTAGTGAATGAATTTGAGGGGGGATTCTCAGTAGACAACG	120
ele.max	TTCCCTACATCGGCAACCAACCTAGTGAATGAATTTGAGGGGGGATTCTCAGTAGACAACG	120
afr.con	TCCCCTATATTGGTCAAAACCTAGTGAATGAATTTGAGGGGGGATTCTCAGTTGACAACC	120
pavo.mut	TCCCCTATATTGGTCAAAACCTAGTGAATGAATTTGAGGGGGGATTCTCAGTTGACAACC	120
tra.bly	TCCCATACATTGGGCAAAACCTAGTGAATGAATTTGAGGGGGGATTCTCAGTTGACAATC	120
tra.sat	TCCCATACATTGGGCAAAACCTAGTGAATGAATTTGAGGGGGGATTCTCAGTTGACAATC	120
tra.cob	TCCCATACATTGGGCAAAACCTAGTGAATGAATTTGAGGGGGGATTCTCAGTTGACAATC	120
tra.tem	TCCCATACATTGGGCAAAACCTAGTGAATGAATTTGAGGGGGGATTCTCAGTTGACAATC	120
arg.arg	TCCCCTATATTGGTCAAAACCTAGTGAATGAATTTGAGGGGGGATTCTCAGTTGACAATC	120
cat.wal	TCCCCTACATCGGACAGACCCCTAGTGAATGAATTTGAGGGGGGATTCTCAGTTGACAACC	120
cro.cro	TCCCCTACATCGGACAGACCCCTAGTGAATGAATTTGAGGGGGGATTCTCAGTTGACAACC	120
sym.ree	TCCCCTACATCGGACAGACCCCTAGTGAATGAATTTGAGGGGGGATTCTCAGTTGACAACC	120
bam.tho	TCCCCTACATCGGACAGACCCCTAGTGAATGAATTTGAGGGGGGATTCTCAGTTGACAACC	120
fra.fra	TCCCCTACATCGGACAGACCCCTAGTGAATGAATTTGAGGGGGGATTCTCAGTTGACAACC	120
ith.cru	TCCCCTACATCGGACAGACCCCTAGTGAATGAATTTGAGGGGGGATTCTCAGTTGACAACC	120
ant.par	TCCCATATATCGGCAAAACCTTGTAGAATGAGCTTGAGGGGGGTTTCTCAGTAGACAATC	120
ant.vir	TCCCATACATCGGCAAAACCTTGTAGAATGAGCTTGAGGGGGGTTTCTCAGTAGACAATC	120
gru.ant.ant	TCCCCTACATCGGCAAAACCTTGTAGAATGAGCTTGAGGGGGGTTTCTCAGTAGACAATC	120
gru.ant.gil	TCCCCTACATCGGCAAAACCTTGTAGAATGAGCTTGAGGGGGGTTTCTCAGTAGACAATC	120
gru.ant.sha	TCCCCTACGCGCGGCAAAACCTTGTAGAATGAGCTTGAGGGGGGTTTCTCAGTAGACAATC	120
gru.leu	TCCCCTACATCGGCAAAACCTTGTAGAATGAGCTTGAGGGGGGTTTCTCAGTAGACAATC	120
gru.can.pra	TCCCATACATCGGCAAAACCTTGTAGAATGAGCTTGAGGGGGGTTTCTCAGTAGACAATC	120
gru.can.row	TCCCATACATCGGCAAAACCTTGTAGAATGAGCTTGAGGGGGGTTTCTCAGTAGACAATC	120
gru.can.tab	TCCCATACATCGGCAAAACCTTGTAGAATGAGCTTGAGGGGGGTTTCTCAGTAGACAATC	120
gru.can.can	TCCCATACATCGGCAAAACCTTGTAGAATGAGCTTGAGGGGGGTTTCTCAGTAGACAATC	120
gru.ame	TCCCATACATCGGCAAAACCTTGTAGAATGAGCTTGAGGGGGGTTTCTCAGTAGACAATC	120
gru.gru	TCCCATACATCGGCAAAACCTTGTAGAATGAGCTTGAGGGGGGTTTCTCAGTAGACAATC	120
gru.mon	TCCCATACATCGGCAAAACCTTGTAGAATGAGCTTGAGGGGGGTTTCTCAGTAGACAATC	120
gru.nig	TCCCATACATCGGCAAAACCTTGTAGAATGAGCTTGAGGGGGGTTTCTCAGTAGACAATC	120
gru.jap	TCCCATACATCGGCAAAACCTTGTAGAATGAGCTTGAGGGGGGTTTCTCAGTAGACAATC	120
cic.boy	TCCCCTACATCGGCAAAACCTTGTAGAATGAGCTTGAGGGGGGTTTCTCAGTAGACAATC	120
rhe.ame	TCCCCTACATCGGCAAAACCTTGTAGAATGAGCTTGAGGGGGGTTTCTCAGTAGACAATC	120
ant.alb	TCCCATACATCGGCAAAACCTTGTAGAATGAGCTTGAGGGGGGTTTCTCAGTAGACAATC	120
fal.fam	TCCCATACATCGGCAAAACCTTGTAGAATGAGCTTGAGGGGGGTTTCTCAGTAGACAATC	120
fal.ver	TCCCATACATCGGCAAAACCTTGTAGAATGAGCTTGAGGGGGGTTTCTCAGTAGACAATC	120
fal.per	TCCCATACATCGGCAAAACCTTGTAGAATGAGCTTGAGGGGGGTTTCTCAGTAGACAATC	120
fal.spa	TCCCATATATCGGCAAAACCTTGTAGAATGAGCTTGAGGGGGGTTTCTCAGTAGACAATC	120
ayc.ame	TCCCATACATCGGCAAAACCTTGTAGAATGAGCTTGAGGGGGGTTTCTCAGTAGACAATC	120
smi.sha	TTCCATACATCGGCAAAACCTTGTAGAATGAGCTTGAGGGGGGTTTCTCAGTAGACAATC	120
vid.cha	TTCCATACATTGGGCAAAACCTTGTAGAATGAGCTTGAGGGGGGTTTCTCAGTAGACAATC	120
chry.pic	TCCCATACATTGGCAATACACTAGTGAATGAATTTGAGGGGGGTTTCTCAGTAGACAATC	120
emy.orb.kur	TCCCATACATCGGCAAAACCTTGTAGAATGAGCTTGAGGGGGGTTTCTCAGTAGACAATC	120
che.mud	TCCCATACATTGGCAACCAACCTAGTGAATGAATTTGAGGGGGGTTTCTCAGTAGACAATC	120
eum.egr	.....	
aep.mel	CAACCCCTNACCCGATTTTTCGCTTTCAGCTTCATCTTTCATTCATTCATTCGCGGACTAG	130
ore.ore	CAACCCCTTACCCGATTTTTCGCTTTCAGCTTCATCTTTCATTCATTCATTCGCGGACTAG	130
add.nas	CAACCCCTTACCCGATTTTTCGCTTTCAGCTTCATCTTTCATTCATTCATTCGCGGACTAG	130
ory.dam	CAACCCCTCAGCCGATTTTTCGCTTTCAGCTTCATCTTTCATTCATTCATTCGCGGACTAG	130
hip.equ	CAACCCCTCAGCCGATTTTTCGCTTTCAGCTTCATCTTTCATTCATTCATTCGCGGACTAG	130
alo.bus	CAACCCCTTACCCGATTTTTCGCTTTCAGCTTCATCTTTCATTCATTCATTCGCGGACTAG	130
sig.lis	CAACCCCTTACCCGATTTTTCGCTTTCAGCTTCATCTTTCATTCATTCATTCGCGGACTAG	130
bea.hun	CAACCCCTCAGCCGATTTTTCGCTTTCAGCTTCATCTTTCATTCATTCATTCGCGGACTAG	130
lum.lun	CAACCCCTCAGCCGATTTTTCGCTTTCAGCTTCATCTTTCATTCATTCATTCGCGGACTAG	130
con.hur	CAACCCCTTACCCGATTTTTCGCTTTCAGCTTCATCTTTCATTCATTCATTCGCGGACTAG	130
amm.les	CTACTTTCAGCCGATTTTTCGCTTTCAGCTTCATCTTTCATTCATTCATTCGCGGACTAG	130
pus.nay	CAACCCCTCAGCCGATTTTTCGCTTTCAGCTTCATCTTTCATTCATTCATTCGCGGACTAG	130







hipp.amp	CCACCCCTTACACGATTCTTTGGCCTTCCACTTTTATTCTTCCATTCTTATCAGAGCACTAG	130
dic.sum	CCACCCCTCACCCTGTTCTTTGGCTTTCCACTTTCATCTCTCCCTTTCATCATCTAGCCCTAG	130
rhin.son	CTACCCCTTACCCGATTCTTTGGCTTTCCACTTTCATCTCTCCCTTTCATCATCTAGCCCTAG	130
cera	CCACACTTACACGATTCTTTGGCCTTTCCACTTTTATTCTACCCCTTTCATCATCAGCCCTGG	130
equu	CCACCCCTTACCCGATTCTTTGGCCTTTCCACTTTTATTCTACCCCTTTCATCATCAGCCCTGG	130
baby.bab	CAACCCCTCAGACGATTCTTTGGCCTTTCCACTTTCATTTTACCTTTTTCATCATCAGCCCTGG	130
phac.afr	CAACCCCTTACACGATTCTTTGGCCTTTCCACTTTTATTCTACCCCTTTCATCATCAGCCCTGG	130
sus.bar	CAACCCCTTACACGATTCTTTGGCCTTTCCACTTTTATTCTACCCCTTTCATCATCAGCCCTGG	130
sus.scr.ewb3	CAACCCCTCAGACGATTCTTTGGCCTTTCCACTTTTATTCTACCCCTTTCATCATCAGCCCTGG	130
lama.gla	CCACCCCTTACACGATTCTTTGGCCTTTCCACTTTTATTCTACCCCTTTCATCATCAGCCCTGG	130
lama.gua	CCACCCCTTACACGATTCTTTGGCCTTTCCACTTTTATTCTACCCCTTTCATCATCAGCCCTGG	130
vic.vic	CCACCCCTTACACGATTCTTTGGCCTTTCCACTTTTATTCTACCCCTTTCATCATCAGCCCTGG	130
cam.bac	CCACCCCTCAGACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
arc.for	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
arc.gaz	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
eum.jub	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
tal.cal	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
odo.ros	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
pho.fasciata	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
pho.gro	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
pho.vit	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
cys.cri	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
hyd.lep	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
lep.wed	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
mir.leo	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
eri.bar	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
mon.sch	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
hela.mal	CGACTCTAACACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
sel.thi	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
ail.ful	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
fel	CGACTCTAACACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
can	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
tal	CGACTCTAACACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
gla.sab	CTACCCCTAACCCGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
gla.vol	CTACCCCTAACCCGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
hyl.pha	CTACCCCTAACCCGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
pet.sec	CTACCCCTAACCCGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
bel.pea	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
pte.mom	CTACCCCTAACACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
gala.demi	CTACCCCTAACACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
pero.pot	CTACCCCTAACACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
gala.mat	CGACCCCTTACTCGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
gala.moh	CTACTCTTACCCGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
oto.gar	CAACCCCTCACCCTGTTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
lor.tar	CAACCCCTCAGACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
nyd.cou	CGACACTCAGACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
mus	CGACCTTGACCCGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
gort	CTACCCCTTACACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
homo	CGACCCCTCAGACGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
dug.dug	CGACCCCTCAGCCGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
ele.max	CAACCCCTAAGCCGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
afr.con	CAACCCCTCAGCCGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
pavo.mut	CAACCCCTCAGCCGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
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tea.cob	CAACCCCTCAGCCGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
tea.tem	CAACCCCTCAGCCGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130
tea.ary	CAACCCCTCAGCCGATTCTTTGGCCTTTCCACTTTCATCTCCCTTTCATCATCAGCCCTGG	130

cat.wal	CAACTCTCACCCGATTCTTCGCCCTTACACTTTCTCTCCTTCCGTAAATTCAGGAATTA	130
cro.cro	CAACCCTCACCCGATTCTTCGCCCTTACACTTTCTCTCCTTCCGTAAATTCAGGAATTA	130
sym.ree	CAACCCTCACCCGATTCTTCGCCCTTACACTTTCTCTCCTTCCGTAAATTCAGGAATTA	130
bam.tho	CAACTCTCACCCGATTCTTCGCCCTTACACTTTCTCTCCTTCCGTAAATTCAGGAATTA	130
fra.fra	CAACCCTCACCCGATTCTTCGCCCTTACACTTTCTCTCCTTCCGTAAATTCAGGAATTA	130
ith.cru	CAACCCTCACCCGATTCTTCGCCCTTACACTTTCTCTCCTTCCGTAAATTCAGGAATTA	130
anc.par	CCACATTAACTCGATTCTTTCACCTTTACACTTTCTCTCCTTCCATTGATAAATATAGGGCTCA	130
anc.vir	CCACATTAACTCGATTCTTTCACCTTTACACTTTCTCTCCTTCCATTGATAAATATAGGGCTCA	130
gru.ant.anc	CCACATTAACTCGATTCTTTCACCTTTACACTTTCTCTCCTTCCATTGATAAATATAGGGCTCA	130
gru.ant.gil	CCACATTAACTCGATTCTTTCACCTTTACACTTTCTCTCCTTCCATTGATAAATATAGGGCTCA	130
gru.ant.sha	CCACATTAACTCGATTCTTTCACCTTTACACTTTCTCTCCTTCCATTGATAAATATAGGGCTCA	130
gru.leu	CCACATTAACTCGATTCTTTCACCTTTACACTTTCTCTCCTTCCATTGATAAATATAGGGCTCA	130
gru.can.pra	CCACATTAAACCCGATTCTTTCACCTTTACACTTTCTCTCCTTCCATTGATAAATATAGGGCTCA	130
gru.can.row	CCACATTAAACCCGATTCTTTCACCTTTACACTTTCTCTCCTTCCATTGATAAATATAGGGCTCA	130
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gru.can.can	CCACATTAAACCCGATTCTTTCACCTTTACACTTTCTCTCCTTCCATTGATAAATATAGGGCTCA	130
gru.ame	CCACATTAAACCCGATTCTTTCACCTTTACACTTTCTCTCCTTCCATTGATAAATATAGGGCTCA	130
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che.mud	CAACCCTAAACCCGATTCTTTCGCCCTTACACTTTCTCTCCTTCCATTGATAATTCAGGACTTA	130
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hig.equ      CCATAGTACACCTACTCTTTCTCCATGAGACAGGCTCCAAACAACCCACAGGAATTTGAT 240
alc.bus      CCATAGTTACCTCTTTATTCCTCCACGAAACAGGATCTTAACAACCCCCACAGGAATCTTCAT 240
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pse.nay      CCATAGTCCACCTACTCTTTCTCCACGAAACAGGATCTTAACAACCCCCACAGGAATTCAGAT 240
cap.ibe      CCATAGTCCACCTCTCTCTTTCTCCACGAAACGGATCTTAACAACCCCCACAGGAATTCAGAT 240
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cap.fal      CCATAGTCCACCTACTCTTTCTCCACGAAACAGGATCTTAACAACCCCCACAGGAATTCAGAT 240
sup.pyt      CCATAGTCCACCTACTCTTTCTCCATGAAACAGGATCTTAACAACCCCCACAGGAATTCAGAT 240
sup.sup      CCTAGTCCACCTATTCTTTCTCCATGAAACAGGATCTTAACAACCCCCACAGGATTCAGAT 240
hem.cau      CTATAGTCCACCTACTCTTTCTCCATGAAACAGGATCTTAACAACCCCCACAGGATTCAGAT 240
bud.tak.tak CCATAGTCCACTTTATTTCTTTCTCCATGAAACAGGATCTTAACAACCCCCACAGGAATTCAGAT 240
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pvi.amm      CCATAGTCCACCTATTCTTTCTTTCTCCATGAAACAGGATCTTAACAACCCCCACAGGAATTCAGAT 240

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bos.tra	CAATAATCCATCTACTCTTCTCCACGAAACAGGATCCAACAATCCAACAGGAATTTCAT	240
bub.min	CAATAGTCCACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
buba.bub	CAATAGTCCACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
tra.ang	TTATGGTCCACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
tra.eur	CCATGGTACACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
kob.ell	CCATAGTCCATCTTCTGTTTCTCCACGAAACAGGATCCAATAATCCACAGGAATTTCAT	240
kob.meg	CTATAGTTCACCTACTTTTTCTCCACGAAACAGGATCTAACAACCCACAGGAATTTCAT	240
red.aru	CTATAGTACACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
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pel.cap	CCATAGTACACCTACTTTTTCTCCACGAAACAGGATCTAATAACCCACAGGAATTTCAT	240
gas.dam	CCATAGTTCACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
our.our	CCACAGTCCACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
ant.cer	CCATAGTACACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
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mos.mos	CCATGGTTTCATCTACTTTTTCTCCACGAAACAGGATCCAATAACCCACAGGAATTTCAT	240
tri.jay	TCCTAGTCCACCTTTTTATTTTTCTCCACGAAACAGGATCCAATAACCCACAGGAATTTCAT	240
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 sup. pyr CAGATGCCGATRAAAAATCCCATTCACCCCTTATTATACCATCAAGACATCTTAGGCGCCA 300  
 sup. sup CAGACATAGACAAAATCCCATTCACCCCTTATTATACCAATCAAGATATCTTAGGCGCTA 300  
 nem. cau CAGATGCCAGATAAAAATCCCATTCACCCCTTATTATACCATTAAGATATCTTAGGAGTCA 300  
 bud. tax. tax CAGATGCCAGACAAAATCCCATTCACCCCTTACTATACCATTAAGACATCTTAGGCGCTA 300  
 pan. hod CCGACACAGATAAAAATCCCGTTTCACCCCTTACTACACCATTAAGACATCTTAGGCGCCA 300  
 ovi. amm CCGACACAGACAAAATCCCGTTTCACCCCTTACTACACCATTAAGACATCTTAGGCGCCA 300  
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 bis. bon CAGACCGCAGACAAAATCCCATTCACCCCTTACTATACCAATTAAGACATCTTAGGAGCCT 300  
 bon. gru CAGACCGCAGATAAAAATCCCATTCACCCCTTACTACACCATTAAGACATCTTAGGAGCCT 300  
 bon. tra CAGACCGCAGATAAAAATCCCATTCACCCCTTACTACACCATTAAGACATCTTAGGAGCCT 300



bub.min	CAGACACAGACAAAATCCCATTTCCACCCCTACTACACCAATTAAGACATTCTAGGCGCCC	300
buba.bub	CAGACACAGACAAAATCCCATTTCCACCCCTATTACACCAATTAAGACATCTAGGCGCCC	300
tra.ang	CAGACATAGACAAAATCCCATTTCCACCCCTATTACACTATCAAGGACATCTAGGCGCCC	300
tra.eur	CRAACATAGACAAAATCCCATTTCCACCCCTACTACACTATTAAGGACATCTAGGCGCCC	300
kob.ell	CAGACATAGATAAAATCCCATTTCCACCCCTACTACACCAATCAAGACATTTCTAGGCGCCC	300
kob.meg	CAGACACAGACAAAATCCCATTTCCACCCCATATTATACCATCAAGATATTTCTAGGCGCCC	300
red.aru	CAGATGTAGACAAAATCCCATTTCCATCCCATACTATATCAAGGACGTCCTAGGCGCCC	300
red.ful	CAGAYATGGACAAAATCCCATTTCCACCCNTACTACACCAATCAAGAYATTTCTAGGCGCCC	300
neo.mos	CAGACGCAGACAAAATCCCATTTCCACCCCTACTACACCAATTAAGACATTTCTAGGCGCCA	300
pel.cap	CCGACATAGACAAAATCCCATTTCCACCCCATACTACACCAATTAAGATATTTCTAGGCGCCT	300
gaz.dam	CAGATGCAGACAAAATCCCATTTCCACCCCTACTACACCAATCAAGACATTTCTAGGAGCAC	300
our.our	CAGATGCAGACAAAGTCCCATTTCCACCCCTACTACACTATCAAGATATCTTAGGAGCTC	300
ant.cer	CAGACGCAGACAAAATCCCATTTCCACCCCTACTACACCAATTAAGACATTTCTAGGCGCCC	300
sai.tac	CAGATTCAGACAAAATCCCATTTCCACCCCTACTACACTATTAAGACATCTTAGGCGCCC	300
mad.kir	CAGACGCAGACGGAATCCCATTTCCGCCCCCTACTACACTATTAAGACATCTTAGGCGCCC	300
rap.mel	CAGATATAGACAAAATCCCATTTCCACCCCTACTACACCAATTAAGACATTTTAGGAGCCCC	300
gaz.gaz	CAGACGCAGACAAAATCCCATTTCCACCCCTACTACACCAATCAAGGACATTTCTAGGAGCAC	300
ant.ame	CAGACGCAGACAAAATCCCATTTCCACCCCTACTACACCAATCAAGACATTTCTAGGAGCAC	300
hyd.ine	CAGATGCAGATAAAATCCCATTTCCATCCCTACTACACCAATTAAGATATTTCTAGGTGTAC	300
mun.mun	CAGATGTAGACAAAATCCCATTTCCATCCCTACTATACCAATTAAGATATTTTAGGTGCCC	300
alc.alc	CAGACGCAGACAAAATCCCATTTCCACCCCTACTACACTATCAAGATATCTTAGGTGCCC	300
cer.ela.kan	CAGACGCAGACAAAATCCCATTTCCATCCCTACTATACCAATTAAGATATCTTAGGCATCT	300
cer.ela.xan	CAGACGCAGACAAAATCCCATTTCCATCCCTACTATACCAATTAAGATATCTTAGGCATCT	300
cer.ela.can	CAGACGCAGACAAAATCCCATTTCCATCCCTACTATACCAATTAAGATATCTTAGGCATCT	300
cer.nip.cent	CGGACGCAGACAAAATCCCATTTCCATCCCTACTACACCAATTAAGATATCTTAGGCATCT	300
cer.nip.yes	CGGACGCAGACAAAATCCCATTTCCATCCCTACTATACCAATTAAGATATCTTAGGCATCT	300
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cer.nip.pul	CGGACGCAGACAAAATCCCATTTCCATCCCTACTATACCAATTAAGATATCTTAGGCATCT	300
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cer.ela.sco	CAGACGCAGACAAAATCCCATTTCCATCCCTATTATACCAATTAAGATATCTTAGGCATCT	300
cer.dam	CAGATGTAGATAAAATCCCATTTCCATCCCTACTACACCAATTAAGATATTTTAGGCATCC	300
ran.tar	CAGACTCAGATAAAATCCCATTTCCATCCCTATTATATCAAGACATTTCTAGGTGTCC	300
mos.fus	CAGATATAGACAAAATCCCATTTCCACCCCTACTACACCAATCAAGACATTTCTAGGTGTCC	300
mos.leu	CAGATATAGACAAAATCCCATTTCCACCCCTACTACACCAATCAAGACATTTCTAGGTGTCC	300
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mos.ber	CAGACATAGACAAAATCCCATTTCCACCCCTACTACACCAATCAAGATATTTCTAGGTATCC	300
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tra.jav	CAGACGCAGACAAAATCCCATTTCCACCCCATACTACACTATTAAGACATTTCTAGGGTTCC	300
trag.nap	CAGACGCAGACAAAGATCCCATTTCCACCCCATACTACACCAATCAAGATGTCTAGGGGCTC	300
bala.acu	CTGACATAGACAAAATCCCATTTCCACCCCTACTACACCAATCAAGACATTTCTAGGGGCTC	300
bala.bon	CTGATATAGACAAAATCCCATTTCCACCCCTATTACACCAATCAAGACATTTCTAGGGGCTC	300
bala.bor	CCGACATAGACAAAATCCCATTTCCACCCCTACTACACCAATCAAGACATTTCTAGGGGCTC	300
bala.edi	CCAACATAGACAAAATCCCATTTCCACCCCTATTACACCAATTAAGACATTTCTAGGGGCTC	300
esch.rob	CCAACATAGACAAAATCCCATTTCCACCCCTACTACACCAATTAAGACATTTCTAGGGGCTC	300
bala.mus	CTGACATAGATAAAATCCCATTTCCACCCCTACTACACCAATTAAGACATTTCTAGGGGCTC	300
mega.nov	CCAACATAGACAAAATCCCATTTCCACCCCTACTACACCAATCAAGACACTTTAGGGGCTC	300
bala.phy	CCGACATAGATAAAATCCCATTTCCACCCCTACCACACCAATTAAGACATTTCTAGGTGCCC	300
cap.mar	CCAACATAGACAAAATCCCATTTCCACCCCTACTACACCAATTAAGACATTTCTAGGGGCTC	300
ceph.com	CCAACATAGACATAATCCCATTTCCACCCCTATTACACCAATTAAGACATTTCTAGGGGCTC	300
ceph.eut	CCAACATAGACATAATCCCATTTCCACCCCTATTACACCAATTAAGACATTTCTAGGGGCTC	300
lage.obl	CCAACATAGACATAATCCCATTTCCACCCCTATTACACCAATTAAGACATTTCTAGGGGCTC	300
ceph.heu	CCAACATAGACATAATCCCATTTCCACCCCTATTACACCAATTAAGACATTTCTAGGGGCTC	300
ceph.hec	CCAACATAGACATAATCCCATTTCCACCCCTATTACACCAATTAAGACATTTCTAGGGGCTC	300
lage.aus	CCAACATAGACATAATCCCATTTCCACCCCTACTACACCAATTAAGACATTTCTAGGGGCTC	300
lage.sru	CCAACATAGACATAATCCCATTTCCACCCCTATTACACCAATTAAGACATTTCTAGGGGCTC	300
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liso.bor	CCAACATAGACATAATCCCATTTCCACCCCTATTACACCAATTAAGACATTTCTAGGGGCTC	300
liso.por	CCAACATAGACATAATCCCATTTCCACCCCTATTACACCAATTAAGACATTTCTAGGGGCTC	300

glo.mac CCAACATAGACATAAATTCCTATTCACCCCTATTATACAAATTAAGACATCCTAGGCGCCC 300  
 glo.mel CCAACATAGACATAAATTCCTATTCACCCCTATTATACAAATTAAGATATCCTAGGCGCCC 300  
 fere.att CCAACATAGACATAAATTCCTATTCACCCCTATTATACAACTAAAGATATCCTAGGTGCCC 300  
 pepo.ele CCAACATAGACATAAATTCCTATTCACCCCTATTATACAAATTAAGACATCCTAGGCGCTC 300  
 gram.gri CCAACATAGACATAAATTCCTATTCACCCCTATTACACAAATTAAGACATCCTAGGCGCCC 300  
 pse.cra CCAACATAGACATAAATTCCTATTCACCCCTATTACACAAATTAAGATATCCTAGGCGCCC 300  
 lage.acu CTAACATAGATATAAATTCCTATTCACCCCTATTATACAAATTAAGATATCCTAGGCGCTT 300  
 orci.bre CCAACATAGATATAAATTCCTATTCACCCCTATTACACAAATTAAGATATCCTAGGCGCCC 300  
 orca.bre CCAACATAGACATAAATTCCTATTCACCCCTATTACATACATTTAAAGACATCCTAGGCGCCC 300  
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 del.tro CCAACATAGACATAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGTGCTT 300  
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 sten.cly CCAATATAGACATAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGTGCTT 300  
 sten.coe CCAATATAGACATAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGTGCTT 300  
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 sten.fro CCAATATAGACATAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGTGCTT 300  
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 lage.alb CCAACATAGATATAAATTCCTATTCACCCCTATTATACAAATCAAAGACATCCTAGGCGCTT 300  
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 sota.flu CCAACATAGATATAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGTGCTT 300  
 del.leu CCAACATAGATATAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGTGCTT 300  
 mono.mon CCAACATAGACATAAATTCCTATTCACCCCTATTATACAAATCAAAGACATCCTAGGCGCTT 300  
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 plat.min CCAACACTGACAAAATTCCTATTCACCCCTATTATACAAATCAAAGACATCCTAGGCGCTT 300  
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 kogi.sim CTGATATAGACAAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGCGCTT 300  
 phys.cat CCAACATAGACAAAATTCCTATTCACCCCTATTATACAAATCAAAGACATCCTAGGCGCTT 300  
 lipo.vex CTAACATAGACAAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGCGCTT 300  
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 bera.bai CCAATATAGATAAAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGCGCTT 300  
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 meso.bid CCGACATAGATAAAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGCGCTT 300  
 meso.den CTGACATAGATAAAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGCGCTT 300  
 hype.amp CTAACATAGACATAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGCGCTT 300  
 meso.par CCAATATAGATAAAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGCGCTT 300  
 pent.bia CCGATATAGACAAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGCGCTT 300  
 hex.lib CTGATATAGACAAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGCGCTT 300  
 hipp.amp CCAACCGCAGACAAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGCGCTT 300  
 dic.sum CTAACATAGACAAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGCGCTT 300  
 shin.son CTAACACAGACAAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGCGCTT 300  
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 baby.bab CAGATATAGACAAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGCGCTT 300  
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 sus.bar CAGACATAGACAAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGCGCTT 300  
 sus.ser.ewb3 CAGACATAGACAAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGCGCTT 300  
 lama.gla CCGATATAGACAAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGCGCTT 300  
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 cam.bar CAGACATAGACAAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGCGCTT 300  
 acc.for CTGACTCAGACAAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGCGCTT 300  
 acc.gaz CTGACTCAGACAAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGCGCTT 300  
 eum.jub CCAACTCAGACAAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGCGCTT 300  
 cal.cal CTGACTCAGACAAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGCGCTT 300  
 odr.egg CTGACTCAGACAAAATTCCTATTCACCCCTATTATACAAATCAAAGATATCCTAGGCGCTT 300

pho.fasciata	CCGACTCAGACAAAAATCCCATTTCCACCCATACTATACAATTTAAAGATATCCTAGGAGCCC	300
pho.gro	CCGACTCAGACAAAAATCCCGCTCCACCCATACTATACAATTTAAAGATATCCTAGGAGCCC	300
pho.vic	CCAATCAGACAAAAATCCCATTTCCACCCCTACTATACAATTTAAAGATATCCTAGGGGCCC	300
cys.cri	CCGACTCAGACAAAAATCCCATTTCCACCCATACTATACAATTTAAAGACATCCTAGGAGCCC	300
hyd.lep	CCAATCAGACAAAAATCCCATTTCCACCCCTACTATACAATTTAAAGACATCCTAGGAGCCC	300
lep.wed	CTGACTCAGACAAAAATCCCATTTCCACCCCTACTATACAATTTAAAGATATCCTAGGAGCCC	300
mir.leo	CCGACTCAGACAAAAATCCCATTTCCACCCATACTATACAATTTAAAGATATCCTAGGAGCCC	300
eri.bar	CCGACTCAGATAAAAAATCCCATTTCCACCCATACTATACAGTCAAGGACATCCTAGGGGCTT	300
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ail.ful	CCAATCAGACAAAAATCCCATTTCCATCCCTATTATACAATTTAAAGATATCCTTGGGCGCTC	300
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can	CAGACTCAGACAAAAATCCCATTTCCACCCCTACTATACAATTTAAAGGATATCCTAGGAGCCT	300
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gla.sab	CTGACTCAGATAAAAAATCCCATTTCCACCCCTATTCTCAATTTAAAGACACCCCTAGGATTCT	300
gla.vol	CTGACTCAGACAAAAATCCCATTTCCACCCCTACTTTCTCAATTTAAAGATATCCTAGGAGCTT	300
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pet.set	CCGATTCAGACAAAAATCCCATTTCCACCCATACTATTCAATTTAAAGATCTCCTAGGGGCCC	300
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pte.mom	CCGAATCCGACAAAAATCCCATTTCCACCCCTACTTTCAATTTAAAGACATTTTTAGGAGCAC	300
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oto.gar	CAGACTCTGACAAAAATCCCATTTCCACCCCTATTACCAATTTAAAGACCTTCTAGGGGCTA	300
lor.tar	CAGACTCTGACAAAAATCCCATTTCCACCCCTACTATACAATTTAAAGATATTCTAGGAGTAA	300
nyc.cou	CAGACTCAGATAAGATTCCCATTTCCACCCCTACTACTCAATTTAAAGACCTCCTAGGAGTGG	300
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homo	CCCATTTCCGATAAAAAATCCCATTTCCACCCCTACTATACAATTTAAAGACGCCCCTCGGCTTAC	300
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afr.con	CCAATTCAGATAAAAAATCCCATTTCCACCCCTACTACTCCCTCAAAGATATCCTAGGCCTAG	300
pavo.mut	CCAATTCAGACAAAAATCCCATTTCCACCCCTACTACTCCCTCAAAGATATCCTAGGCCTAA	300
tra.bly	CTAATCTGACAAAAATCCCATTTCCACCCCTACTACTCCCTCAAAGATATCCTAGGCCTAA	300
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sym.ree	CTAATCTGACAAAAATCCCATTTCCACCCCTACTACTCCCTCAAAGATATCCTAGGCCTAG	300
bam.tho	CTAATCTGACAAAAATCCCATTTCCACCCCTACTACTCCCTCAAAGACATCCTAGGCCTAG	300
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ant.par	CAAATCTGCGATAAAAAATCCCATTTCCACCCCTACTTTTCTTAAAGATATCCTAGGATTCA	300
ant.vir	CAAATCTGCGATAAAAAATCCCATTTCCACCCCTACTTTTCTTAAAGATATCCTAGGATTCA	300
gru.ant.ant	CAAATCTGCGATAAAAAATCCCATTTCCACCCCTACTTTTCTTAAAGATATCCTAGGATTCA	300
gru.ant.gil	CAAATCTGCGATAAAAAATCCCATTTCCACCCCTACTTTTCTTAAAGATATCCTAGGATTCA	300
gru.ant.jhu	CAAATCTGCGATAAAAAATCCCATTTCCACCCCTACTTTTCTTAAAGATATCCTAGGATTCA	300
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gru.ame	CAAATCTGCGATAAAAAATCCCATTTCCACCCCTACTTTTCTTAAAGATATCCTAGGATTCA	300
gru.gri	CAAATCTGCGATAAAAAATCCCATTTCCACCCCTACTTTTCTTAAAGATATCCTAGGATTCA	300

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gru.mon      CAAACTGCGATAAAATTCATTCCACCCCTATTTTTCCTTAAAAGATATCCTAGGATTCA 300
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gru.jap      CAAACTGTGATAAAATCCCATTCACCCCTATTTTTCCTTAAAAGATATCTTAGGATTTA 300
cic.boy      CAAACTGCGACAAAATTCATTCCACCCCTACTTCTCCCTCAAAGATATCCTAGGCCTTA 300
rhe.ame      CTCACTCTGACAAAATCCCATTCACCCCTACTTCTCCCTAAAAGATGCCCTAGGACTAG 300
ant.alb      CCAACTGCGACAAAATCCCATTCACCCCTACTTTGCCCTAAAAGACATCCTAGGATTCA 300
fal.fam      CAAACTGCGATAAAATTCATTCCATCCCTATTACTCTCTCAAAGACCTCTTAGGATTCA 300
fal.ver      CAAACTGCGACAAAATCCCATTCATCCCTACTACTCTCTCAAAGACCTTTTAGGAGTCA 200
fal.per      CAAATTTGCGACAAAATCCCATTCACCCCTACTACTCTCTCAAAGATATCCTAGGATTTA 300
fal.spa      CAAACTGTGACAAAATCCCATTCACCCCTACTACTCTCTCAAAGACCTCCTAGGTTTTA 300
ayt.ame      CAGACTGCGACAAAATCCCATTTCCACCCCTACTTCTCCTTCAAAGACATCCTAGGATTTA 300
smi.sha      CTAACTCCGATAAAATCCCATTCACCCCTACTTCTCCATAAAAGACATTCTAGGCTTTG 300
vid.cha      CAGACTGTGACAAAATTCATTCCACCCCTACTACACCACAAAGGACATCCTAGGCTTCG 300
chry.pic     CAAACACTGACAAAATCCCATTCACCCCTATTTCTCATATAAAGACCTTTTAGGCGTCA 300
emy.orb.kur  CAAACACCGATAAAATCCCTTTCCATCCCTACTTCTCATACAAAGACCTATTAGGACTCA 300
che.mud      CAAATACCGACAAAATCCCTTTCCACCCCTACTTCTCTTACAAAGACTTACTAGGACTCA 300
eum.egr      CTAGCACAGATAAGGTGCCATTCACCCCTATTACACATACAAAGACCTTCTTGGTTTCA 300
*          *          *          *          *          *          *          *
aep.mel      TATTAATAATTCTAGTCCTAATACTCCTAGTACTATTTCATACCCGACCTACTAGGAGACC 360
ore.ore      TATTACTAATTCTAGCTTTTATTACTCTTAGTATTATTTCACACCTGACCTACTTGGAGACC 360
add.nas      TACTACTAATTCTAGTCCTGACTACTACTAGTATTATTTCACACCCGACCTACTTGGAGACC 360
ory.dam      TACTACTAATCCTAGCCCTTATGTTGCTAGTACTATTTCGCACCCGACCTACTTGGAGACC 360
hip.equ      TACTACTAATTCTAGCCCTCATACTACTAGTACTATTTCGCACCCGACCTACTTGGAGACC 360
alc.bus      TATTACTAATCCTAGCCCTCATACTACTAGTACTATTTCGCACCCGACCTGCTCGGAGACC 360
sig.lic      TATTACTAATTCTAGCCCTCATACTACTAGTACTATTTCGCACCCGACCTGCTCGGAGACC 360
bea.hun      TACTACTAATTCTAGCCCTCATATTACTAGTACTATTTCGCACCCGACCTGCTCGGAGACC 360
dam.lun      TACTACTAATTCTAGCCCTCATACTACTAGTACTATTTCGCACCCGACCTGCTCGGAGACC 360
con.tau      TATTACTAATTCTAGCCCTAATACTACTAGTACTATTTCGCACCCGACCTGCTCGGAGACC 360
amm.ler      TGCTACTAATCCTCACCCTCAGACTACTAGTACTATTTCACACCCGACCTACTCGGGGACC 360
pse.nay      CACTGCTAATCCTCGCCCTGATATTACTAGTATTATTTCACACCCGACCTACTCGGAGACC 360
cap.ibe      TGCTACTAATTCTTGCTCTAATATTACTAGTACTATTTCACACCCGACCTACTCGGGGACC 360
hem.jem      TACTACTAATTCTTGCTCTAATATTACTAGTACTATTTCACACCCGACCTACTTGGAGACC 360
cap.fal      TACTACTAATTCTCGCCCTGATGCTACTAGTACTATTTCACACCTGACCTACTCGGAGACC 360
rup.pyr      TACTACTAATCCTCACCCTTATACTACTGGTACTATTTCACACCTGACCTACTCGGAGACC 360
rup.rup      TACTACTAATCCTCACCCTTATACTACTGGTACTATTTCACACCTGACCTACTCGGAGACC 360
nem.cau      TACTACTAATCCTCACCCTTATTTACTGGTACTATTTCACACCTGACCTACTCGGAGACC 360
bud.tax.tax  TACTACTAATCCTCGTCCCTCATGTTGCTAGTACTATTTCACACCCGACCTACTCGGAGACC 360
pan.hod      TACTACTAATCCTAATCCTCATATTACTAGTACTATTTCACACCCGACCTACTCGGAGACC 360
ovi.amm      TCCTACTAATCCTCACCCTCATACTACTAGTACTATTTCACACCCGACCTACTCGGAGACC 360
ovi.vig      TCCTACTAATCCTCATCCTCATGCTGCTAGTACTATTTCACACCCGACCTACTCGGAGACC 360
cap.cri      TGCTACTAATCCTCACCCTCATACTACTAGTACTGTTTCACACCCGACCTACTCGGAGACC 360
ovi.mos      TACTACTAATCCTTACCCTTATACTACTAGTATTATTTCACACCCGACCTACTTGGAGACC 360
ore.ame      TACTACTCATCCTCACCCTTATACTACTAGTATTATTTCACACCCGACCTACTCGGAGACC 360
cep.dor      TACTACTCATTCTAGCCCTAATAATCCTAGTATTATTTCACACCCGACCTACTTGGAGACC 360
cep.max      TATTACTTATTCTAGCCCTAATAATCCTAGTACTATTTCACACCCGACCTACTCGGAGACC 360
bis.bon      TATTACTAATTCTAATCCTAATACTACTAGTACTATTTCACACCCGACCTCCTCGGAGACC 360
bos.gru      TATTACTAATTCTAGCCCTAATAACTTCTGCTACTATTTCACACCCGACCTCCTCGGAGACC 360
bos.tra      TACTACTTATTCTAGCCCTAATAATACTAGTACTATTTCACACCCGACCTCCTCGGAGACC 360
bub.min      TGCTATTAATCCTAGCCCTAATAACTATTAGTACTATTTCACACCCGACCTCCTCGGGGACC 360
buba.bub     TACTATTAATCCTAGCCCTAATAACTATTAGTACTATTTCACACCCGACCTCCTCGGGGACC 360
tra.ang      TACTATTAATCCTAGCCCTAATAACTAGTACTATTTCACACCTGACCTCCTCGGAGACC 360
tra.eur      TACTGCTAATCCTAATCCTAATCCTAGTACTATTTCACACCCGACCTCCTCGGAGACC 360
kob.ell      TACTACTAATCCTAGTCCCTAATACTCCTAGTATTATTTCACACCCGACCTACTTGGAGACC 360
kob.meg      TCCTATTAATCCTAATACTAATACTCCTAGTACTATTTCACACCCGACCTACTTGGAGACC 360
red.aru      TACTGCTAATCCTAGTCCCTAATCCTAATCCTAGTATTATTTCACACCCGACCTACTCGGAGACC 360
red.ful      TACTACTAATCCTCGCCCTAACACTATTAGTACTATTTCACACCCGACCTACTCGGAGACC 360
neo.mos      TCCTACTAATCCTAGTCCCTAACACTATTAGTATTATTTCACACCCGACCTACTTGGAGACC 360

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del.cap	TACTCCTAATCTTAACCCCTACTAGCACTGACCCTATTCACTCCAGACCTACTAGGAGACC	350
del.tro	TACTCCTAATCTTAACCCCTACTAGCACTGACCCTATTCACTCCCGACCTACTAGGAGACC	350
del.del	TACTCCTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
sten.cly	TACTCCTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
sten.coe	TACTCCTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
tur.adu	TACTCCTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAAACC	350
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saus.chi	TACTCCTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
sten.lon	TACTCCTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
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lage.alb	TACTTTTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
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sota.flu	TACTCCTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
del.leu	TACTCCTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
mono.mon	TCTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
plat.gan	TCTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
plat.min	TCTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
kogi.bre	TACTGCTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
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phys.cat	TACTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
lipo.vex	TCTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
phoc.sin	TACTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
bera.bai	TACTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
niph.car	TACTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
meso.eur	TACTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
meso.bid	TACTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
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meso.per	TATTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
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sus.bar	TATTCTAATACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
sus.scr.ewb1	TATTCTAATACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
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lage.alb	CCGATAACTATACCCGAGCAAAATCCACTAAGCACTCCTGCACACATCAAACCAGAAATGGT	420
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sus.scr.ewb3	CAGACAACCTACACCCGAGCAAAACCCACTAAACACCCCAACCCATATTAACCAGAAATGAT	420
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sal.cal	CAGACAACCTATATTCGAGCAAAACCCCTCAGCACTCCACCACATATTAACCTGAATGAT	420
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pho.fasciata	CCGACAACCTACACCCCTGCCAATCCCTAAGTACCCCAACACATATCAAAGCCGGAATGAT	420
pho.gro	CCGACAACCTATATCCCTGCCAATCCCTAAGTACCCCAACACATATCAAAGCTGAATGGT	420
pho.vit	CCGACAACCTATATCCCTGCCAATCCCTAAGTACCCCAACACATATTAACCTGAATGAT	420
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mir.leo	CCGACAACCTACACCCCTGCCAATCCCTAAGTACCCCAACACATATTAAGCCGGAATGAT	420
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non.sch	CTGACAACCTACATCCCTGCCAATCCCTAAGTACCCCAACACATTAACCTGAATGAT	420
rel.mal	CTGACAACCTACATCCCTGCCAATCCCTAAGTACCCCAACACATTAACCTGAATGAT	420
rel.chi	CTGATAACTATACCCCGGCAAAACCCACTGAGCACCCCAACCCACATCAAACCTGAATGAT	420
vil.ful	CTGATAACTATATTCCTGCTAACCCTAAGTACCCCAACACATTAACCTGAATGAT	420
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al	CAGACAATTACATCCCTGCCAATCCCTAAGTACCCCAACACATTAACCTGAATGAT	420
la.sab	CAGACAACCTATACCCGAGCAAAACCCACTTAACACCCCTCCCATATTAACCTGAATGAT	420
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yl.pha	CTGACAACCTACACCCCGGCAAAACCCACTTAACACCCCTCCCATATTAACCTGAATGAT	420

aep.mel	ACTTCCTGTTNGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
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ory.dam	ATTTTCTATTTCGCATATGCGATCCTTACGATCAATCCCCAATAAACTAGGAGG	472
hip.equ	ATTTTTTATTTCGCGTACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
alc.bus	ATTTTCTATTTCGCATATGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
sig.lic	ATTTTCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
bea.hun	ATTTTCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
dam.lun	ATTTTCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
con.tau	ACTTCCTATTTCGCATATGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
amm.ler	ACTTCCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
pse.nay	ACTTCCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
cap.ibe	ATTTTCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
hem.jem	ATTTTCTATTTCGCATACGCGATCCTACGATCAATCCCCAATAAACTAGGAGG	472
cap.fal	ACTTCCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
rup.pyr	ATTTTCTATTTCGCATATGCGATCCTACGATCAATCCCCAATAAACTAGGAGG	472
rup.rup	ATTTTCTATTTCGCATATGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
nem.cau	ATTTTCTATTTCGCATATGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
bud.tax.tax	ATTTTCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
pan.hod	ACTTCCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
ovi.amm	ACTTCCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
ovi.vig	ATTTTCTATTTCGCATATGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
cap.cri	ACTTCCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
ovi.mos	ACTTCCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
ore.ame	ACTTCCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
cep.dor	ACTTCCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
cep.max	ATTTTCTATTTCGCGTACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
bis.bon	ACTTCCTATTTCGCATANGCAATTTTACGGTCAATCCCCAATAAACTAGGAGG	472
bos.gru	ACTTCCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
bos.tra	ATTTTCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
bub.min	ACTTCCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
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tra.eur	ACTTCCTATTTCGCATATGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
kob.ell	ACTTCCTATTTCGCATATGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
kob.meg	ATTTTCTATTTCGCATACGCAATTTTACGGTCAATCCCCAATAAACTAGGAGG	472
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red.ful	ACTTCCTATTTCGCATATGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
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pel.cap	ATTTTCTATTTCGCATATGCGATCCTACGATCAATCCCCAATAAACTAGGAGG	472
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our.our	ATTTTCTATTTCGCATACGCAATTTCTCGATCAATCCCCAATAAACTAGGAGG	472
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ran.tar	ACTTCTATTTGCATACGCAATCCTACGATCAATTCCCAATAAACTAGGAGG	472
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mos.leu	ATTTCTATTTGCATATGCCATTCTACGATCAATTCCCAACAAACTAGGAGG	472
mos.chr	ACTTCTATTTGCATATGCCATTCTACGATCAATTCCCAACAAACTAGGAGG	472
mos.ber	ACTTCTATTTGCATATGCCATTCTACGATCAATTCCCAACAAACTAGGAGG	472
mos.mos	ACTTCTATTTGCATATGCCATTCTACGATCAATTCCCTAATAAACTAGGAGG	472
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bala.bor	ATTTCTATTTGCATACGCAATCCTACGATCAATCCCAACAAACTAGGAGG	472
bala.edi	ATTTCTATTTGCATACGCAATCCTACGATCAATCCCAACAAACTAGGAGG	472
esch.rob	ATTTCTATTTGCATACGCAATCCTACGATCAATCCCAACAAACTAGGAGG	472
bala.mus	ATTTCTATTTGCATACGCAATCCTACGATCAATCCCAACAAACTAGGAGG	472
mega.nov	ATTTCTATTTGCATACGCAATCCTACGATCAATCCCAACAAACTAGGAGG	472
bala.phy	ATTTCTATTTGCATACGCAATCCTACGATCAATCCCAACAAACTAGGAGG	472
cap.mar	ACTTCTATTTGCATATGCCATTCTACGATCAATTCCCTAATAAACTAGGAGG	472
ceph.com	ACTTCTATTTGCATATGCCATTCTACGATCAATTCCCAATAAACTAGGAGG	472
ceph.eut	ACTTCTATTTGCATATGCCATTCTACGATCAATTCCCTAATAAACTAGGAGG	472
lage.obl	ACTTCTATTTGCATATGCCATTCTACGATCAATTCCCTAATAAACTAGGAGG	472
ceph.heu	ACTTCTATTTGCATATGCCATTCTACGATCAATTCCCTAATAAACTAGGAGG	472
ceph.hec	ACTTCTATTTGCATATGCCATTCTACGATCAATTCCCTAATAAACTAGGAGG	472
lage.aus	ATTTCTATTTGCATATGCCATTCTACGATCAATTCCCTAATAAACTAGGAGG	472
lage.cru	ATTTCTATTTGCATATGCCATTCTACGATCAATTCCCTAATAAACTAGGAGG	472
lage.obs	ATTTCTATTTGCATATGCCATTCTACGATCAATTCCCTAATAAACTAGGAGG	472
lisso.bor	ACTTCTATTTGCATACGCAATCCTACGATCAATTCCCTAATAAACTAGGAGG	472
lisso.per	ACTTCTATTTGCATACGCAATCCTACGATCAATTCCCTAATAAACTAGGAGG	472
glo.mac	ATTTCTATTTGCATATGCCATTCTACGATCAATTCCCAATAAACTAGGAGG	472
glo.mel	ATTTCTATTTGCATATGCCATTCTACGATCAATTCCCAATAAACTAGGAGG	472
fere.att	ATTTCTATTTGCATATGCCATTCTACGATCAATTCCCTAATAAACTAGGAGG	472
pepo.ele	ATTTCTATTTGCATATGCCATTCTACGATCAATTCCCAATAAACTAGGAGG	472
gram.gri	ATTTCTATTTGCATATGCCATTCTACGATCAATTCCCAATAAACTAGGAGG	472
pse.cra	ATTTCTATTTGCATATGCCATTCTACGATCAATTCCCAACAAACTAGGAGG	472
lage.acu	ACTTCTATTTGCATACGCAATCCTACGATCAATCCCAATAAACTAGGAGG	472
orci.bre	ACTTCTATTTGCATACGCAATCCTACGATCAATCCCAATAAACTAGGAGG	472
orca.bre	ACTTCTATTTGCATACGCAATCCTACGATCAATCCCAATAAACTAGGAGG	472
del.cap	ACTTCTATTTGCATACGCAATCCTACGATCAATCCCAATAAACTAGGAGG	472
del.tro	ACTTCTATTTGCATACGCAATCCTACGATCAATCCCAATAAACTAGGAGG	472
del.del	ACTTCTATTTGCATATGCCATTCTACGATCAATCCCTAATAAACTAGGAGG	472
sten.cly	ACTTCTATTTGCATATGCCATTCTACGATCAATCCCTAATAAACTAGGAGG	472
sten.coe	ACTTCTATTTGCATATGCCATTCTACGATCAATCCCTAATAAACTAGGAGG	472
tur.adu	ACTTCTATTTGCATACGCAATCCTACGATCAATCCCTAATAAACTAGGAGG	472
sten.fro	ATTTCTATTTGCATACGCAATCCTACGATCAATCCCTAATAAACTAGGAGG	472
saus.chi	ATTTCTATTTGCATACGCAATCCTACGATCAATCCCTAATAAACTAGGAGG	472
sten.lon	ACTTCTATTTGCATACGCAATCCTACGATCAATCCCTAATAAACTAGGAGG	472
curs.tru	ATTTCTATTTGCATATGCCATTCTACGATCAATCCCTAATAAACTAGGAGG	472
lage.alb	ATTTCTATTTGCATACGCAATCCTACGATCAATCCCAACAAACTAGGAGG	472
sten.bre	ATTTCTATTTGCATATGCCATTCTACGATCAATCCCTAATAAACTAGGAGG	472
sota.flu	ACTTCTATTTGCATACGCAATCCTACGATCAATCCCAACAAACTAGGAGG	472
del.leu	ATTTCTATTTGCATACGCAATCCTACGATCAATCCCAACAAACTAGGAGG	472
mono.mon	ATTTCTATTTGCATACGCAATCCTACGATCAATCCCAACAAACTAGGAGG	472
plac.gan	ATTTCTATTTGCATACGCAATCCTACGATCAATCCCAATAAACTAGGAGG	472
plac.min	ATTTCTATTTGCATACGCAATCCTACGATCAATCCCAATAAACTAGGAGG	472
kogi.bre	ATTTCTATTTGCATATGCCATTCTACGATCAATCCCTAATAAACTAGGAGG	472

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mun.mun	CCGACAATTATACCCAGCAAACCCACTCAATACACCCCCCTCACATCAAGCCTGAATGAT	420
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cer.ela.kan	CAGACAACCTATACCCAGCAAATCCACTCAATACACCCCCCTCACATTAACCCTGAATGAT	420
cer.ela.xan	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCACATTAACCCTGAATGAT	420
cer.ela.can	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCACATTAACCCTGAATGAT	420
cer.nip.cent	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCACATTAACCCTGAATGAT	420
cer.nip.yes	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCACATTAACCCTGAATGAT	420
cer.nip.ker	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCACATTAACCCTGAATGAT	420
cer.nip.pul	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCACATTAACCCTGAATGAT	420
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cer.ela.sco	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
cer.dam	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
ran.tar	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
mos.fus	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
mos.leu	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
mos.chr	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
mos.ber	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
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tra.jav	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
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bala.acu	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
bala.bon	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
bala.bor	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
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esch.rob	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
bala.mus	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
mega.nov	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
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cap.mar	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
ceph.com	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
ceph.eut	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
lage.obl	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
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lage.obs	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
lisso.bor	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
lisso.per	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
glo.mac	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
glo.mel	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
fere.att	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
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pse.cra	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
lage.acu	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
orci.bre	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
orca.bre	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
del.cap	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
del.tro	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
del.del	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
sten.cly	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
sten.coe	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
tur.adu	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
sten.fro	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
aus.chi	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420
sten.lon	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCTGAATGAT	420

kogi.sim	ACTTTCTATTCCGCATACGCCATTCTACGATCAATTCCTAACAAACTGGGAGG	472
phys.cat	ATTTCCCTATTCCGCGTACGCCATCCTACGATCTGTCCCCAATAAACTAGGAGG	472
lipo.vex	ATTTCCCTCTTCGCATACGCCAATCTACGATCAATTCCTAACAAACTAGGAGG	472
phoc.sin	ATTTCCCTCTTCGCATACGCCAATCTACGATCAATTCCTAACAAACTAGGAGG	472
bera.bai	ACTTCCTGTTCCGCATACGCCAATCTACGATCAATTCCTAACAAACTAGGAGG	472
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meso.eur	ACTTCCTATTCCGCATACGCCAATCTACGATCAATTCCTAACAAACTAGGAGG	472
meso.bid	ATTTCCCTATTCCGCATACGCCAATCTACGATCAATTCCTAACAAACTAGGAGG	472
meso.den	ATTTCTTATTTCGCATACGCCAATCTACGATCAATTCCTAACAAACTAGGAGG	472
hype.amp	ATTTCTTATTTCGCATACGCCAATCTACGATCAATTCCTAACAAACTAGGAGG	472
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pont.bla	ATTTCCCTATTCCGCTACGCCATCCTACGATCAATTCCTAACAAACTAGGAGG	472
hex.lib	ATTTCCCTGTTCCGCATACGCCAATCTCCGATCAATTCCTAACAAACTAGGAGG	472
hipp.amp	ATTTCCCTGTTCCGCTACGCCAATCTCCGATCAATTCCTAACAAACTAGGAGG	472
dic.sum	ACTTCCTATTCCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
rhin.son	ATTTCCCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
cera	ACTTTCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
equu	ATTTCCCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
baby.bab	ACTTCCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
phac.afr	ACTTCCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
sus.bar	ACTTCCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
sus.scr.ewb3	ATTTCTTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
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lama.gua	ACTTCCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
vic.vic	ATTTCCCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
cam.bac	ATTTCTTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
arc.for	ATTTCTTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
arc.gaz	ATTTCTTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
eum.jub	ATTTCCCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
zal.cal	ATTTCCCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
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pho.fasciata	ACTTTCTATTTCGCTACGCCAATCTACGATCAATTCCTAACAAACTAGGAGG	472
pho.gro	ACTTTCTATTTCGCTACGCCAATCTACGATCAATTCCTAACAAACTAGGAGG	472
pho.vit	ACTTCCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
cys.cri	ACTTCCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
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lep.wed	ATTTCCCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
mir.leo	ATTTCCCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
eri.bar	ATTTCCCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
mon.sch	ACTTCCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
hela.mal	ACTTTCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
sel.chi	ACTTTCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
ail.ful	ATTTCCCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
fel	ACTTCCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
can	ATTTCTTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
tal	ACTTCCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
gla.sab	ACTTTCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
gla.vol	ACTTTCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
hyl.pha	ACTTTCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
pet.set	ACTTTCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
bel.pea	ACTTTCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
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gala.demi	ACTTTCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
pero.pot	ACTTTCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
gala.mat	ACTTTCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
gala.moh	ACTTTCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
oto.gar	ATTTCCCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472
los.car	ATTTCCCTATTTCGCTACGCCAATCTACGATCCATTCCTAACAAACTAGGAGG	472

PRIMER 'mc5869'

Results for RID 984593689-1224-27770



BLASTN 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593689-1224-27770<sup>1</sup>

Query-

(128 letters)

Database: Sequences from complete mitochondrial genomes  
129 sequences; 3,164,247 total letters

If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQs](#)

Taxonomy reportsDistribution of 80 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments





## Sequences producing significant alignments:

(bits) Value

ref NC_001700.1	Felis catus mitochondrion, complete genome	365	e-101
ref NC_001325.1	Phoca vitulina mitochondrion, complete genome	198	1e-51
ref NC_002008.1	Canis familiaris mitochondrion, complete g...	190	4e-49
ref NC_001602.1	Halichoerus grypus mitochondrion, complete...	180	3e-46
ref NC_000884.1	Cavia porcellus complete mitochondrial genome	176	5e-45
ref NC_001808.1	Ceratotherium simum mitochondrion, complet...	155	2e-41
ref NC_001892.1	Myoxus glis mitochondrion, complete genome	153	8e-38
ref NC_001788.1	Equus asinus mitochondrion, complete genome	151	3e-37
ref NC_002073.1	Orycteropus afer complete mitochondrial ge...	149	1e-36
ref NC_001821.1	Dasyus novemcinctus mitochondrion, comple...	141	3e-34
ref NC_001779.1	R.unicornis complete mitochondrial genome	135	2e-32
ref NC_001569.1	Mus musculus mitochondrion, complete genome	133	7e-32
ref NC_000889.1	Hippopotamus amphibius mitochondrion, comp...	125	2e-29
ref NC_001640.1	Equus caballus mitochondrion, complete genome	125	2e-29
ref NC_001794.1	Macropus robustus mitochondrion, complete ...	123	7e-29
ref NC_000845.1	Sus scrofa mitochondrion, complete genome	121	3e-28
ref NC_001665.1	Rattus norvegicus mitochondrial genome	121	3e-28
ref NC_001567.1	Bos taurus mitochondrion, complete genome	121	3e-28
ref NC_001643.1	Pan troglodytes mitochondrion, complete ge...	117	4e-27
ref NC_001941.1	Ovis aries mitochondrion, complete genome	109	1e-24
ref NC_002391.1	Talpa europaea mitochondrion, complete genome	103	7e-23
ref NC_001913.1	Oryctolagus cuniculus mitochondrion, compl...	103	7e-23
ref NC_001644.1	Pan paniscus mitochondrion, complete genome	101	3e-22
ref NC_001807.2	Human mitochondrion, complete genome	99	4e-21
ref NC_001601.1	Balaenoptera musculus mitochondrion, compl...	98	4e-21
ref NC_002009.1	Artibeus jamaicensis mitochondrion, comple...	96	2e-20
ref NC_001645.1	Gorilla gorilla mitochondrion, complete ge...	92	2e-19
ref NC_001321.1	Balaenoptera physalus mitochondrion, compl...	90	1e-18
ref NC_001610.1	Didelphis virginiana mitochondrion, comple...	80	9e-16
ref NC_002082.1	Hylobates lar mitochondrion, complete genome	70	9e-13
ref NC_001727.1	Crossostoma lacustre mitochondrion, comple...	70	9e-13
ref NC_001804.1	Latimeria chalumnae mitochondrion, complet...	68	4e-12
ref NC_000880.1	Vidua chalybeata mitochondrion, complete g...	66	1e-11
ref NC_002069.1	Corvus frugilegus mitochondrion, complete ...	64	6e-11
ref NC_000886.1	Chelonia mydas mitochondrial DNA, complete...	62	2e-10
ref NC_001646.1	Pongo pygmaeus mitochondrion, complete genome	62	2e-10
ref NC_001606.1	Cyprinus carpio mitochondrion, complete ge...	62	2e-10
ref NC_000890.1	Mustelus manazo mitochondrion, complete ge...	60	9e-10
ref NC_001323.1	Gallus gallus mitochondrion, complete genome	60	9e-10
ref NC_002079.1	Carassius auratus mitochondrion, complete ...	58	3e-09
ref NC_000934.1	Loxodonta africana mitochondrion, complete...	56	1e-08
ref NC_000878.1	Falco peregrinus mitochondrion, complete g...	56	1e-08
ref NC_000846.1	Rhea americana mitochondrion, complete genome	56	1e-08
ref NC_002196.1	Ciconia boyciana mitochondrion, complete g...	54	5e-08
ref NC_001960.1	Salmo salar mitochondrion, complete genome	54	5e-08
ref NC_001778.1	Polypterus ornatipinnis mitochondrion, com...	54	5e-08
ref NC_002083.1	Pongo pygmaeus abelii mitochondrion, compl...	52	2e-07
ref NC_001953.1	Struthio camelus complete mitochondrial ge...	52	2e-07
ref NC_001947.1	Pelomedusa subrufa mitochondrion, complete...	52	2e-07
ref NC_001770.1	Arbacia lixula mitochondrion, complete genome	52	2e-07

## Alignments

cmpseq_0	1	tgaatctgaggaggcttctcagtagacaaagctaccccgacacgattctcttgccttccac	60
NC_001700	15524	.....g..g.....c.....a.....g.....	15583
NC_001325	15580	.....a..t.....t.....a..t..a.....c.....	15639
NC_002008	14673	.....c.....g.....a.....a.....t.....t.....	14729
NC_001602	15553	.....a..t.....t.....a..t..a..g.....c.....	15612
NC_000884	14650	.....g..g.....c.....a.....t.....t.....	14709
NC_001808	14662	.....a..t..c..t.....c..a..c.....c.....t.....	14721
NC_001892	14654	.....c.....c.....c.....t.....c.....c.....	14713
NC_001788	14671	.....c..a.....c.....c.....c.....c.....	14730
NC_002078	14663	.....c.....c.....c.....a..a..a.....c.....	14716
NC_001821	14657	.....c.....c.....c.....a..t..a.....c.....	14716
NC_001779	14664	.....a.....c.....c.....c.....c.....c.....	14723
NC_001562	14625	.....c.....g.....c.....c.....c.....c.....	14684
NC_000892	14658	.....c.....c.....c.....c.....c.....c.....	14717
NC_001640	14674	.....c..a.....c.....c.....c.....c.....	14711
NC_001794	14670	.....g..a.....c.....c.....c.....c.....c.....	14727



[illegible]

tmpseq_0	61	ttcatcctccatttatcatctcagctctagcagcagctccacctctattctctcacgag	120
NC_001700	15584	.....t.....c.t.....ct.....g...a.....t.....t.....a	15643
NC_001325	15640	.....a.....cg.ag.a.t.....a.....ac.....a.....a.....a	15699
NC_002008	14730	.....c.t.c.c.....g.....at.....a.....t.....a.....a	14789
NC_001502	15613	.....a.....cg.ag.a.t.....a.....a.....a.....a.....a	15672
NC_000884	14710	..t..t.....c.....a.c.c.....tgat.....t.....c.....	14769
NC_001808	14722	..t.....c.c.....t.....at.c.....atcac.....a.....a	14781
NC_001892	14714	..t..t..a..c.c.t..tg...c...t.at.....c.....c.....a	14773
NC_001788	14731	..t..t..a..c.....a.....c.g.t.atc.....t..a.....c.....a	14790
NC_002078	14717	..t.....g.....t..tg.....tat.....t.....t.....a.....a	14776
NC_001821	14717	..t.....t.a.....t.....a.....a.c.t.t.....gt.....a.....a	14776
NC_001779	14724	..t.....c.c.c.t.....ct.....c.....a.c.....a.....a.....a	14783

NC	001569	14685	.....c.a.....c...g.g.c.....acc..c.....c.....a	14744
NC	000889	14718	..t..c.....cg.c...a...acc..t..a.....c..t..a	14777
NC	001640	14734	.....a..c..c.....a..c.g..cc..a..cc..a.....t.....a	14793
NC	001794	14730	..t.....a.....c.....a.....c..c..t.....t.....a.....	14789
NC	001794	14730	.....a.....c.....a.....c..c..t.....t.....a.....	14745
NC	000845	15888	..t.....g.....c.....ca.c.c.c.....c..a..t.....g.....a	15947
NC	001665	14670	.....c.....c..t...g.c.c.c..t...acc..a..t..t..t.....c.....a	14729
NC	001567	15060	.....t.....ac..ad..c..cat.....a.....c.....a	15119
NC	001643	14711	..t..t.a..c..c.....a.....c..a..a..c..t..t.....c..a.....a	14770
NC	001941	14705	..t..cc.c.....c.....g.....c..c..cat..t.....a..c.....a	14764
NC	002391	14731	.....c.g.....t..cg.g..a.....cg..t.....gt.....c.....a	14790
NC	001913	14721	.....t.g.....t.....c.....a.....a.....a.....a.....a	14740
NC	001644	14712	..t.....a..c..c..t...a...c...a..a..c..t..t.....c.....a	14771
NC	001807	15293	.....t.g..c..c..t..cg.....c.....a..c.....t.g.....a	15352
NC	001601	15156	.....t..c..c..c..t..at.....acc.....a..c.....a	15215
NC	002009	14596	..cc.a.....c..c..cg..a.....t..at.....cc.....t..a.....a	14755
NC	001645	14715	..t.....a..c..c.....a.....c..a..a..cc.....t.....c..a.....a	14774
NC	001331	15159	..t.....c..c..c.....c..t..at.....acc.....ca..t.....a	15218
NC	001610	14723	..c..c.....c.....c..t..a..t..t..a..t..t.....t.....a	14782
NC	002045	14713	.....a..c..c..t...a.g..c.....cc.g.....t.....a.....	14772
NC	001727	15824	.....a.....c.....a.....g.....c.....cc.g.....t.....a.....	15826
NC	001727	15872	.....a.....c.....a.....g.....c.....cc.g.....t.....a.....	15843
NC	001904	14887	.....c.....g.....t.....c.....a.....a.....a.....a.....a	14702

NC_001804	14928	.....g..c.....t...	14948
NC_000880	15567	.....ac.....a.....a	15591
NC_002069	14244	...c...a..c...g..a...g...gc...a..ct...t.....aacc.....a	14303
NC_000886	14778	...	14780
NC_001646	14737	.....a..a..t..c.....ta.....a..a..cc..t.....a	14796
NC_001606	15839	...	15841
NC_000890	14901	..	14902
NC_002079	15842	...c....a.....	15862
NC_000934	14693	.....t.....	14708
NC_000878	14264	...c.a.....	14277
NC_000846	14235	.....a.....a	14246
NC_000846	14187	...	14189
NC_001960	15930	...	15932
NC_001778	14823	.....t.....	14833
NC_001953	14170	...c....c.....	14184
NC_001770	15120	...	15122

tmpseq_0	121	acaggatctaaccaacccctcaggaatagtagtccgactcagacaaaattccattccaccca	180
NC_001700	15644	.....tac.....t.....c.....	15703
NC_001325	15700	.....a.....c.....ca.....c.....g	15759
NC_002008	14790	..c....c.....t.....cac...a.....c.....t.....t	14849
NC_001602	15673	.....a.....c.....ca..c.....c.....g	15732
NC_000884	14770	.....a.....a.....c..aac..a....c.....c.....t	14829
NC_001808	14782	.....c..t.....a.....ccc...a..at.....c.....t	14841
NC_001892	14774	.....g..t.....a.....t..aac..a..a.....c.....g	14833
NC_001788	14791	.....c.....ccc...t..at.....c.....t.....t	14850
NC_002078	14777	.....t..t.....t..t.....a..t.....c..t.....t	14836
NC_001821	14777	.....a.....a.....t..ctcg..aa..at.....c..c.....g	14836
NC_001779	14784	.....g..c.....a.....tcc...a..at.....c.....t.....c	14843
NC_001569	14745	.....a.....aa.....t..aac..a..tg...t.....t.....c	14804
NC_000889	14778	.....c.....aa.....cccc..aa..g.....c.....c	14837
NC_001640	14794	.....t.....ccc.....tatg.....c.....t	14853
NC_001794	14790	..c..t.....a..t.....caacc.....c.....t	14849
NC_000845	15948	..c....c.....ta..c.....ctc...a..at.....t.....t	16007
NC_001665	14730	.....a..t.....a.....t..aac.....g.....c.....t...	14789
NC_001567	15120	.....c..c.....aa.....tccc..a..gt.....c.....c	15179
NC_001643	14771	.....a..t.....ct.....cacc...c.....a..c.....c	14830
NC_001941	14765	.....c.....a.....tcc...g..a...t.....c.....c	14824
NC_002391	14791	.....a.....a.....	14814
NC_001913	14815	.....t.....c.....c.....c	14840
NC_001644	14772	.....a..t.....ct.....cacc...c....c.....a..c.....c	14831
NC_001807	15353	..g....a.....ct.....cacc...c..t..c.....ca..c.....t	15412
NC_001601	15216	.....c.....a.....tccc...t..at...t.....c.....c	15275
NC_002009	14756	.....a.....c..tcc...a..c.....t.....c.....c	14815
NC_001645	14775	.....a.....tcc...c..cccc...c.....t.....ca..c.....c	14834
NC_001321	15219	.....c.....a.....c..ccc.....at...t.....c.....c	15278
NC_001610	14783	.....a..g...t..aa...cc...a.....t.....c.....c	14842

NC_002082	14773	.....a.....t.....c...ctcc...c..ac.....cg..c.....c	14832
NC_001727	15884	.....c..c.....g...cc..aac.....g.....t.....ct..c.....	15943
NC_001804	14949	.....c.....	14965
NC_000880	15592	.....a.....t..aac.....tcc...a...gt.....c.....c	15651
NC_002069	14304	.....c..a.....gct...c..tccc...a...gc.....c.....c	14363
NC_001646	14797	.....a..t.....	14814
NC_001323	15531	.....t.....t.....t.....t.....t.....t.....t.....t	15561
NC_002079	15939	.....t.....t.....t.....t.....t.....t.....t.....t	15961
NC_000934	14786	.....t.....t.....t.....t.....t.....t.....t.....t	14812
NC_000878	14363	.....t.....t.....t.....t.....t.....t.....t.....t	14383
NC_000846	14247	..c..g..c.....t.....c.....tcc...t.....c.....c	14306
NC_002196	16371	.....t.....t.....t.....t.....t.....t.....t.....t	16391
NC_002083	14858	.....t.....t.....t.....t.....t.....t.....t.....t	14866
NC_001953	14269	.....t.....t.....t.....t.....t.....t.....t.....t	14289

tmpseq_0	181	cactacacacatcaagatattccgggctctcagtagtactaattccatgcaactcatattacttc	240
NC_001700	15704	.....c.....c.....a..t.....g..tc...a.....	15763
NC_001325	15760	.....c.....c.....a..gggc...c..t..c..t...tc...a..c.....	15817
NC_002079	14850	.....g.....	14872
NC_001602	15733	.....c.....t.....c.....	15755
NC_001602	15784	.....a.....	15772

NC_000884	14810	..t.....	14846
NC_001808	14842	.....c.....aa..t..c.c.....ac.cgcc..a	14901
NC_001892	14834	..t.....t.....c..a.....a..cc....c..tt.cccc.....acc..a	14893
NC_001788	14851	.....t.....c.....a..a.....	14882
NC_001788	15080		15095
NC_002078	14837	.....	14853
NC_001821	14837	.....t.....t.....	14859
NC_001779	14844	.....c.....	14866
NC_001569	14805	.....t.....	14827
NC_000889	14838	..t.....g..c.....	14860
NC_001640	14854	..t..t.....t.....c.....	14876
NC_001640	15085		15098
NC_001794	14850	..t..t..t.....	14867
NC_000845	16008	.....t..t.....	16024
NC_001665	14790	..t..t.....t.....	14806
NC_001567	15180	.....t..c..t..g..c..t.....c.....t.....t..a.....a	15219

ag

NC_001643	14831	.....	14853
NC_001941	14825	..t.....c..t.....c.....	14847
NC_001913	14841	.....	14857
NC_001644	14832	.....c.....	14854
NC_001807	15413	.....	15429
NC_001601	15276	.....t.....	15292
NC_002009	14816	.....t..t..t.....	14835
NC_001645	14835	.....c.....a.....	14863
NC_001321	15279	..c.....t.....	15295
NC_001610	14843	.....t..c..a.....	14865
NC_002082	14833	.....t.....c.....	14855
NC_001727	15944	....	15947
NC_000880	15652	.....	15659
NC_002069	14364	.....t.....	14381
NC_001323	15562	.....t..ct.....c..t.....	15588
NC_002079	15962	....	15965
NC_000934	14813	.....	14817
NC_000878	14384	.....t..tc.....	14406
NC_000846	14307	....	14310
NC_002196	16392	.....t..t..cc.....a.....	16421
NC_002083	14867	.....c.....a.....	14895
NC_001953	14290	.....	14293

cmpseq_0	241	gtccattatccaccagacctgttaggagaccggataaactacatccctcgccaaacctccca	300
NC_001700	15764	.....t.....c.....a..c.....a.....t..	15823
NC_001325	15820	..g.....c.....a..c.....t.....	15867
NC_002008	14914	.....t.....c.....a.....a.....c.....a.....c...	14969
NC_001602	15793	..a.....c.....a..g.....c.....t..c...	15852
NC_000884	14900	.....c.....a.....a.....ca..c.....g..g	14949
NC_001808	14902	..t.....a..cc.....t..c.....c.....t.....	14960
NC_001892	14894	..t.....c.....t..a.....c.....c.....a...	14953
NC_002078	14909	.....a.....	14928
NC_000845	16071	.....ac.....a..c.....c.....a..a.....a...	16127
NC_001567	15240	..a.....g..c.....cc..c.....a.....c.....a.....	15272
NC_001913	14901	.....t.....a.....a..c.....c.....c.....t	14950
NC_001644	1484		1492
NC_001807	15476	.....cc.....c.....a..c..t..t..c..ca.....cc..	15532
NC_002009	14880	.....t.....cc.....a..c..t..t..t..a..a..c..a..t	14935
NC_001645	14898	.....cc.....a..c.....c..ta.....c.....	14954
NC_001610	14907	.....t..t.....t..c..t..t..c..a..t..t..c..t	14962
NC_002082	14950		14952
NC_001804	15071	.....a..c.....a.....a.....	15108
NC_000886	14980	.....a..c.....t..c..a..a.....	15017
NC_002196	16454	.....ca.....ac.....a..g..t..c..c.....a.....	16507
NC_001950	16155	.....	16169

cmpseq_0	301	aatcccccccccataccaagcctgaac	328
NC_001700	15824	.....t..a.....	15871
NC_002008	14970	..c.....a.....t.....	14975
NC_001602	15853	..gc.....a.....	15872
NC_000884	14950	.....	14954
NC_001922	14754	..g.....	14770

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NC 001779	3081	.....	3094
NC 000845	16128	..c.....a.....	16144
NC 001911	14961	.....	14980
NC 001644	1493	...c.....	1501
NC 001807	15533	..c.....c.....c....	15560
NC 002009	14936	.....c.....a....	14963
NC 001645	14955	.gc.....a.....c....	14974
NC 001610	14963	..c.....g..c.....a....	14990
NC 002082	14953	..c.....c.....	14972
NC 001960	16170	gt...t..a..t.....	16197
NC 001951	14426	.....c....	14437

Database: Sequences from complete mitochondrial genomes

Posted date: Jun 28, 2000 10:56 AM

Number of letters in database: 3,164,247

Number of sequences in database: 129

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3  
 Gap Penalties: Existence: 5, Extension: 2  
 Number of Hits to DB: 788  
 Number of Sequences: 129  
 Number of extensions: 788  
 Number of successful extensions: 168  
 Number of sequences better than 10.0: 77  
 length of query: 328  
 length of database: 3,164,247  
 effective HSP length: 15  
 effective length of query: 313  
 effective length of database: 3,162,312  
 effective search space: 989803656  
 effective search space used: 989803656  
 T: 0  
 A: 30  
 X1: 6 (11.9 bits)  
 X2: 15 (29.7 bits)  
 S1: 12 (24.3 bits)  
 S2: 14 (28.2 bits)

Table 4



BLASTN 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997). "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593400-28182-3122

Query=

(328 letters)

Database: nt

807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reportsDistribution of 50 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



## Sequences producing significant alignments:

	Score (bits)	E Value
gb AY005809.1  Panthera pardus cytochrome b gene, partial c...	603	e-170
gb AF051054.1 AF051054 Panthera tigris sumatrae isolate Su1...	527	e-147
gb AF051053.1 AF051053 Panthera tigris tigris isolate 87 mi...	527	e-147
gb AF051050.1 AF051050 Panthera tigris corbetti isolate C2 ...	476	e-132
gb AF051049.1 AF051049 Panthera tigris corbetti isolate C1 ...	476	e-132
gb AF051025.1 AF051025 Panthera tigris tigris isolate 89 cy...	460	e-127
gb AF051024.1 AF051024 Panthera tigris tigris isolate 88 cy...	460	e-127
gb AF051023.1 AF051023 Panthera tigris tigris isolate 87 cy...	460	e-127
gb AF051022.1 AF051022 Panthera tigris tigris isolate 86 cy...	460	e-127
gb AF051021.1 AF051021 Panthera tigris tigris isolate 85 cy...	460	e-127
gb AF051018.1 AF051018 Panthera tigris tigris isolate 82 cy...	460	e-127
gb AF051051.1 AF051051 Panthera tigris corbetti isolate C3 ...	452	e-125
gb AF051048.1 AF051048 Panthera tigris sumatrae isolate Su1...	452	e-125
gb AF051047.1 AF051047 Panthera tigris sumatrae isolate Su9...	452	e-125
gb AF051046.1 AF051046 Panthera tigris sumatrae isolate Su7...	452	e-125
gb AF051045.1 AF051045 Panthera tigris sumatrae isolate Su6...	452	e-125
gb AF051044.1 AF051044 Panthera tigris sumatrae isolate Su5...	452	e-125
gb AF051042.1 AF051042 Panthera tigris sumatrae isolate Su3...	452	e-125
gb AF051041.1 AF051041 Panthera tigris sumatrae isolate Su2...	452	e-125
gb AF051040.1 AF051040 Panthera tigris sumatrae isolate Su1...	452	e-125
gb AF051039.1 AF051039 Panthera tigris altaica isolate S15 ...	452	e-125
gb AF051038.1 AF051038 Panthera tigris altaica isolate S14 ...	452	e-125
gb AF051037.1 AF051037 Panthera tigris altaica isolate S13 ...	452	e-125
gb AF051036.1 AF051036 Panthera tigris altaica isolate S12 ...	452	e-125
gb AF051035.1 AF051035 Panthera tigris altaica isolate S11 ...	452	e-125
gb AF051034.1 AF051034 Panthera tigris altaica isolate S10 ...	452	e-125
gb AF051033.1 AF051033 Panthera tigris altaica isolate S8 c...	452	e-125
gb AF051032.1 AF051032 Panthera tigris altaica isolate S7 c...	452	e-125
gb AF051031.1 AF051031 Panthera tigris altaica isolate S6 c...	452	e-125
gb AF051030.1 AF051030 Panthera tigris altaica isolate S5 c...	452	e-125
gb AF051029.1 AF051029 Panthera tigris altaica isolate S4 c...	452	e-125
gb AF051028.1 AF051028 Panthera tigris altaica isolate S3 c...	452	e-125
gb AF051027.1 AF051027 Panthera tigris altaica isolate S2 c...	452	e-125
gb AF051026.1 AF051026 Panthera tigris altaica isolate S1 c...	452	e-125
gb AF051020.1 AF051020 Panthera tigris tigris isolate 84 cy...	452	e-125
gb AF051019.1 AF051019 Panthera tigris tigris isolate 83 cy...	444	e-122
gb AF051043.1 AF051043 Panthera tigris sumatrae isolate Su4...	444	e-122
emb X82301.1 MIPTCYTB P.tigris mitochondrial cytochrome b gene	440	e-121
gb AF051052.1 AF051052 Panthera leo cytochrome b (cytb) gen...	438	e-121
emb X82100.1 MIPLCYTBG P.leo mitochondrial cytochrome b gene	399	e-106
db AB004238.1 AB004238 Felis catus mitochondrial DNA for c...	381	e-103
db AB004237.1 AB004237 Felis catus mitochondrial DNA for c...	377	e-102
emb X82296.1 MIFDCYTB F.domesticus mitochondrial cytochrome...	365	1e-98
ref NC_001700.1  Felis catus mitochondrion, complete genome	363	1e-98
gb U20753.1 FCU20753 Felis catus mitochondrion, complete ge...	276	7e-72
gb AF125145.1 AF125145 Viverricula indica cytochrome b gene...	270	4e-70
gb AF125144.1 AF125144 Chrotogale owstoni cytochrome b gene...	255	7e-66
gb AF154975.1 AF154975 Martes martes specimen voucher AF175...	255	7e-66
db AB051237.1 AB051237 Martes martes mitochondrial cytb ge...	246	6e-63
gb AF125149.1 AF125149 Viverra zibetha cytochrome b gene...		

## Alignments

cmpseq_0	1	tgaatctgaggaggctcttcagtagacaaagctaccctgacacgattctcttgcctctccac	60
AY005809	39	.....g.....c.....	98
AF051054	487	.....g.....c.....	546
AF051053	487	.....g.....c.....	546
AF051050	487	.....g.....c.....	546
AF051049	487	.....g.....c.....	546
AF051025	487	.....g.....c.....	546
AF051024	487	.....g.....c.....	546
AF051023	487	.....g.....c.....	546
AF051022	487	.....g.....c.....	546
AF051021	487	.....g.....c.....	546
AF051018	487	.....g.....c.....	546
AF051051	487	.....g.....c.....	546
AF051048	487	.....g.....c.....	546
AF051047	487	.....g.....c.....	546

AF051046	487	.....g..t.....	546
AF051045	487	.....g..t.....	546
AF051044	487	.....g..t.....	546
AF051042	487	.....g..t.....	546
AF051041	487	.....g..t.....	546
AF051040	487	.....g..t.....	546
AF051039	487	.....g..t.....	546
AF051038	487	.....g..t.....	546
AF051037	487	.....g..t.....	546
AF051036	487	.....g..t.....	546
AF051035	487	.....g..t.....	546
AF051034	487	.....g..t.....	546
AF051033	487	.....g..t.....	546
AF051032	487	.....g..t.....	546
AF051031	487	.....g..t.....	546
AF051030	487	.....g..t.....	546
AF051029	487	.....g..t.....	546
AF051028	487	.....g..t.....	546
AF051027	487	.....g..t.....	546
AF051026	487	.....g..t.....	546
AF051020	487	.....g..t.....	546
AF051019	487	.....g..t.....	546
AF051043	487	.....g..t.....	546
X82301	487	.....g..t.....	546
AF051052	487	.....g..t.....	546
X82300	490	.....g..t.....	546
A3004238	487	.....g..t.....	546
A3004237	487	.....g..t.....	546
X82296	487	.....g..t.....	546
NC 001700	15524	.....g..g.....	15583
U20753	15524	.....g..g.....	15583
AF125145	357	.....t.....	416
AF125144	357	.....t.....	416
AF154975	487	.....g.....	546
A3051237	487	.....g.....	546
AF125149	357	.....g.....	416
cmpseq_0	61	ttcatccttccattttatcatctcagctctagcagcagtcacacccctctattcccttcacgag	120
AX005809	99	.....g.....	159
AF051054	547	.....g.....	606
AF051053	547	.....g.....	606
AF051050	547	.....g.....	606
AF051049	547	.....g.....	606
AF051025	547	.....g.....	606
AF051024	547	.....g.....	606
AF051023	547	.....g.....	606
AF051022	547	.....g.....	606
AF051021	547	.....g.....	606
AF051018	547	.....g.....	606
AF051051	547	.....g.....	606
AF051048	547	.....g.....	606
AF051047	547	.....g.....	606
AF051046	547	.....g.....	606
AF051045	547	.....g.....	606
AF051044	547	.....g.....	606
AF051042	547	.....g.....	606
AF051041	547	.....g.....	606
AF051040	547	.....g.....	606
AF051039	547	.....g.....	606
AF051038	547	.....g.....	606
AF051037	547	.....g.....	606
AF051016	547	.....g.....	606
AF051015	547	.....g.....	606
AF051014	547	.....g.....	606
AF051013	547	.....g.....	606
AF051012	547	.....g.....	606
AF051011	547	.....g.....	606
AF051010	547	.....g.....	606
AF051029	547	.....g.....	606
AF051027	547	.....g.....	606

AF051026	547	.....g.....g.....c.....a	606
AF051020	547	.....g.....g.....c.....a	606
AF051019	547	.....g.....g.....c.....a	606
AF051043	547	....c.....g.....g.....c.....a	606
X82101	547	....c.....g.....g.....c.....a	606
AF051052	547	.....g.....g.....c.....a	606
X82100	547	.....g.....g.....c.....a	606
AB004238	547	.....c.....c.....c.....a	606
AB004237	547	.....c.....c.....c.....a	606
X82296	547	.....c.....c.....c.....a	606
NC 001700	15584	.....c.....c.....c.....g.....a.....c.....a	15643
U20753	15584	.....c.....c.....c.....g.....a.....c.....a	15643
AF125145	417	.....c.....c.....c.....c.....a.....a.....a	476
AF125144	417	.....c.....c.....c.....c.....a.....a.....a	476
AF154975	547	.....g.....c.....c.....a.....c.....c.....a	606
AB051237	547	.....g.....c.....c.....a.....c.....c.....a	606
AF125149	417	.....c.....c.....c.....c.....a.....a.....a	476
cmpseq_0	121	acaggatctaacacccccccaggaatagtatccgactcagacaaaattccattccaccca	180
AY005809	159	.....c.....c.....c.....c.....c.....c.....c	218
AF053054	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053053	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053050	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053049	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053025	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053024	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053023	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053022	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053021	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053019	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053051	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053048	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053047	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053046	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053045	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053044	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053042	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053041	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053040	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053039	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053038	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053037	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053036	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053035	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053034	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053033	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053032	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053031	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053030	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053029	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053028	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053027	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053026	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053020	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053019	607	.....c.....c.....c.....c.....c.....c.....c	666
AF053043	607	.....c.....c.....c.....c.....c.....c.....c	666
X82101	607	.....c.....c.....c.....c.....c.....c.....c	666
AF051052	607	.....c.....c.....c.....c.....c.....c.....c	666
X82100	607	.....c.....c.....c.....c.....c.....c.....c	666
AB004238	607	.....c.....c.....c.....c.....c.....c.....c	666
AB004237	607	.....c.....c.....c.....c.....c.....c.....c	666
X82296	607	.....c.....c.....c.....c.....c.....c.....c	15703
NC 001700	15644	.....c.....c.....c.....c.....c.....c.....c	15703
U20753	15644	.....c.....c.....c.....c.....c.....c.....c	536
AF125145	477	.....c.....c.....c.....c.....c.....c.....c	536
AF125144	477	.....c.....c.....c.....c.....c.....c.....c	666
AF154975	607	.....c.....c.....c.....c.....c.....c.....c	666
AB051237	607	.....c.....c.....c.....c.....c.....c.....c	666
AF125142	477	.....c.....c.....c.....c.....c.....c.....c	536
cmpseq_0	181	cattccacaccccaagatccctgggcccctcagtcacacccctagcactccatccctcc	240



AY005809	219	.....c.....	278
AF053054	667	.....c.....a.....	726
AF053053	667	.....c.....a.....	726
AF053050	667	.....c.....a.....c.....	726
AF053049	667	.....c.....a.....c.....	726
AF053029	667	.....c.....a.....c.....	726
AF053024	667	.....c.....a.....c.....	726
AF053023	667	.....c.....a.....c.....	726
AF053022	667	.....c.....a.....c.....	726
AF053021	667	.....c.....a.....c.....c.....	726
AF053018	667	.....c.....a.....c.....c.....	726
AF053051	667	.....c.....a.....c.....	726
AF053048	667	.....c.....a.....c.....g.....	726
AF053047	667	.....c.....a.....c.....g.....	726
AF053046	667	.....c.....a.....c.....g.....	726
AF053045	667	.....c.....a.....c.....g.....	726
AF053044	667	.....c.....a.....c.....g.....	726
AF053042	667	.....c.....a.....c.....g.....	726
AF053041	667	.....c.....a.....c.....g.....	726
AF053040	667	.....c.....a.....c.....g.....	726
AF053039	667	.....c.....a.....c.....	726
AF053038	667	.....c.....a.....c.....	726
AF053037	667	.....c.....a.....c.....	726
AF053036	667	.....c.....a.....c.....	726
AF053035	667	.....c.....a.....c.....	726
AF053034	667	.....c.....a.....c.....	726
AF053033	667	.....c.....a.....c.....	726
AF053032	667	.....c.....a.....c.....	726
AF053031	667	.....c.....a.....c.....	726
AF053030	667	.....c.....a.....c.....	726
AF053029	667	.....c.....a.....c.....	726
AF053028	667	.....c.....a.....c.....	726
AF053027	667	.....c.....a.....c.....	726
AF053026	667	.....c.....a.....c.....	726
AF053020	667	.....c.....a.....c.....	726
AF053019	667	.....c.....a.....c.....	726
AF053043	667	.....c.....a.....c.....g.....	726
X82301	667	.....c.....a.....c.....g.....	726
AF053052	667	.....c.....a.....c.....	726
X82300	667	.....c.....a.....c.....	726
AB004238	667	.....c.....a.....c.....g.....	726
AB004237	667	.....c.....a.....c.....g.....	726
X82296	667	.....c.....a.....c.....g.....	726
NC 001700	15704	.....c.....a.....c.....g.....	15763
U20753	15704	.....c.....a.....c.....g.....	15763
AF125145	537	.....c.....a.....c.....c.....c.....a.....g.....a	596
AF125144	537	.....c.....a.....c.....c.....c.....a.....g.....a	596
AF154975	667	.....c.....a.....g.....c.....c.....c.....a.....a	726
AB051237	667	.....c.....a.....g.....c.....c.....c.....a.....a	726
AF125149	537	.....c.....a.....c.....c.....c.....c.....a.....g.....a	596
cmpseq_0	241	gtccctacccaccagacctgctaggagaccctgataaactacatccctgccaaccctcta	100
AY005809	279	.....c.....	338
AF053054	727	.....a.....g.....c.....	786
AF053053	727	.....a.....g.....c.....	786
AF053050	727	.....a.....c.....c.....	786
AF053049	727	.....a.....c.....c.....	786
AF053029	727	.....a.....c.....c.....	786
AF053024	727	.....a.....c.....c.....	786
AF053023	727	.....a.....c.....c.....	786
AF053022	727	.....a.....c.....c.....	786
AF053021	727	.....a.....c.....c.....	786
AF053018	727	.....a.....c.....c.....	786
AF053051	727	.....a.....c.....c.....	786
AF053048	727	.....a.....c.....c.....	786
AF053047	727	.....a.....c.....c.....	786
AF053046	727	.....a.....c.....c.....	786
AF053045	727	.....a.....c.....c.....	786
AF053044	727	.....a.....c.....c.....	786
AF053043	727	.....a.....c.....c.....	786
AF053042	727	.....a.....c.....c.....	786
AF053041	727	.....a.....c.....c.....	786
AF053040	727	.....a.....c.....c.....	786
AF053039	727	.....a.....c.....c.....	786
AF053038	727	.....a.....c.....c.....	786
AF053037	727	.....a.....c.....c.....	786
AF053036	727	.....a.....c.....c.....	786
AF053035	727	.....a.....c.....c.....	786
AF053034	727	.....a.....c.....c.....	786
AF053033	727	.....a.....c.....c.....	786
AF053032	727	.....a.....c.....c.....	786
AF053031	727	.....a.....c.....c.....	786
AF053030	727	.....a.....c.....c.....	786
AF053029	727	.....a.....c.....c.....	786
AF053028	727	.....a.....c.....c.....	786
AF053027	727	.....a.....c.....c.....	786
AF053026	727	.....a.....c.....c.....	786
AF053020	727	.....a.....c.....c.....	786
AF053019	727	.....a.....c.....c.....	786
AF053043	727	.....a.....c.....c.....	786
X82301	727	.....a.....c.....c.....	786
AF053052	727	.....a.....c.....c.....	786
X82300	727	.....a.....c.....c.....	786
AB004238	727	.....a.....c.....c.....	786
AB004237	727	.....a.....c.....c.....	786
X82296	727	.....a.....c.....c.....	786
NC 001700	727	.....a.....c.....c.....	786
U20753	727	.....a.....c.....c.....	786
AF125145	727	.....a.....c.....c.....	786
AF125144	727	.....a.....c.....c.....	786
AF154975	727	.....a.....c.....c.....	786
AB051237	727	.....a.....c.....c.....	786
AF125149	727	.....a.....c.....c.....	786

<u>AF053040</u>	727	.....a.....c.....	786
<u>AF053039</u>	727	.....a.....c.....c.....c.....	786
<u>AF053038</u>	727	.....a.....c.....c.....c.....	786
<u>AF053037</u>	727	.....a.....c.....c.....c.....	786
<u>AF053036</u>	727	.....a.....c.....c.....c.....	786
<u>AF053035</u>	727	.....a.....c.....c.....c.....	786
<u>AF053034</u>	727	.....a.....c.....c.....c.....	786
<u>AF053033</u>	727	.....a.....c.....c.....c.....	786
<u>AF053032</u>	727	.....a.....c.....c.....c.....	786
<u>AF053031</u>	727	.....a.....c.....c.....c.....	786
<u>AF053030</u>	727	.....a.....c.....c.....c.....	786
<u>AF053029</u>	727	.....a.....c.....c.....c.....	786
<u>AF053028</u>	727	.....a.....c.....c.....c.....	786
<u>AF053027</u>	727	.....a.....c.....c.....c.....	786
<u>AF053026</u>	727	.....a.....c.....c.....c.....	786
<u>AF053020</u>	727	.....a.....c.....c.....c.....	786
<u>AF053019</u>	727	.....a.....c.....c.....c.....	786
<u>AF053043</u>	727	.....a.....c.....c.....c.....	786
<u>X82301</u>	727	.....a.....c.....c.....c.....	786
<u>AF053052</u>	727	.....a.....c.....c.....c.....c.....c.....	786
<u>X82300</u>	727	.....a.....c.....c.....c.....c.....	786
<u>AB004238</u>	727	.....c.....c.....a..c.g.....a.....c.....	786
<u>AB004237</u>	727	.....c.....c.....a..c.....a.....c.....	786
<u>X82296</u>	727	.....c.....c.....a..c.....a.....c.....	786
<u>NC 001700</u>	15764	.....c.....c.....a..c.....a.....c.....	15823
<u>U20753</u>	15764	.....c.....c.....a..c.....a.....c.....	15823
<u>AF125145</u>	597	.....c.....c.....a.....c.....c.....	650
<u>AF125144</u>	597	..c.....c.....c.....a..c.....c.....a.....	656
<u>AF154975</u>	727	..a.....c.....c.g.....a..c.....c.....a..c	786
<u>AB051237</u>	727	..a.....c.....c.g.....a..c.....c.....a..c	786
<u>AF125149</u>	597	.....c.....cc.....a.....c.....c.....	656
<u>cmpseq_0</u>	301	aataccccccccatcatcaagccggaat	329
<u>AY005809</u>	339	.....	366
<u>AF053054</u>	787	..c.....	808
<u>AF053053</u>	787	..c.....	808
<u>AF053050</u>	787	.....c.....c.....	814
<u>AF053049</u>	787	.....c.....c.....	814
<u>AF053025</u>	787	.....c.....c.....	814
<u>AF053024</u>	787	.....c.....c.....	814
<u>AF053023</u>	787	.....c.....c.....	814
<u>AF053022</u>	787	.....c.....c.....	814
<u>AF053021</u>	787	.....c.....c.....	814
<u>AF053018</u>	787	.....c.....c.....	814
<u>AF053051</u>	787	.....c.....c.....	814
<u>AF053048</u>	787	.....c.....c.....	814
<u>AF053047</u>	787	.....c.....c.....	814
<u>AF053046</u>	787	.....c.....c.....	814
<u>AF053045</u>	787	.....c.....c.....	814
<u>AF053044</u>	787	.....c.....c.....	814
<u>AF053042</u>	787	.....c.....c.....	814
<u>AF053041</u>	787	.....c.....c.....	814
<u>AF053040</u>	787	.....c.....c.....	814
<u>AF053039</u>	787	.....c.....c.....	814
<u>AF053038</u>	787	.....c.....c.....	814
<u>AF053037</u>	787	.....c.....c.....	814
<u>AF053035</u>	787	.....c.....c.....	814
<u>AF053035</u>	787	.....c.....c.....	814
<u>AF053034</u>	787	.....c.....c.....	814
<u>AF053033</u>	787	.....c.....c.....	814
<u>AF053032</u>	787	.....c.....c.....	814
<u>AF053031</u>	787	.....c.....c.....	814
<u>AF053030</u>	787	.....c.....c.....	814
<u>AF053029</u>	787	.....c.....c.....	814
<u>AF053028</u>	787	.....c.....c.....	814
<u>AF053027</u>	787	.....c.....c.....	814
<u>AF053026</u>	787	.....c.....c.....	814
<u>AF053020</u>	787	.....c.....c.....	814
<u>AF053019</u>	787	.....c.....c.....	814
<u>AF053043</u>	787	.....c.....c.....	814
<u>X82301</u>	787	.....c.....c.....	814

<u>AF051052</u>	787	.gc.....a.....	812
<u>X82100</u>	787	.gc.....a.....	814
<u>AB004238</u>	787	.....c..a.....	814
<u>AB004237</u>	787	.....c..a.....	814
<u>X82296</u>	787	.....c..a.....	814
<u>NC 001700</u>	15824	.....c..a.....	15851
<u>U20753</u>	15824	.....c..a.....	15851
<u>AF125144</u>	657	..c.....	664
<u>AF154975</u>	787	..c..a..a.....	803
<u>AB051237</u>	787	..c..a..a.....	803
<u>AF125149</u>	657	..c.....	664

Database: nt

Posted date: Mar 2, 2001 12:20 AM

Number of letters in database: 2,861,827,885

Number of sequences in database: 807,597

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 460542

Number of Sequences: 807597

Number of extensions: 460542

Number of successful extensions: 22671

Number of sequences better than 10.0: 6487

length of query: 328

length of database: 2,861,827,885

effective HSP length: 20

effective length of query: 308

effective length of database: 2,847,675,945

effective search space: 877084191060

effective search space used: 877084191060

T: 0

A: 10

X1: 6 (11.9 bits)

X2: 15 (29.7 bits)

S1: 12 (24.3 bits)

S2: 19 (38.2 bits)

**Table 5.** Reference animals and the allocated code numbers included in the study

SN.	Code number	Name of the animal	Zoological name
1	bhz25t	Indian tiger	<i>Panthera tigris tigris</i>
2	bhz26t	Indian tiger	<i>Panthera tigris tigris</i>
3	bhz30t	Indian tiger	<i>Panthera tigris tigris</i>
4	bhz45t	Indian tiger	<i>Panthera tigris tigris</i>
5	bhz56t	Indian tiger	<i>Panthera tigris tigris</i>
6	bhz63t	Indian tiger	<i>Panthera tigris tigris</i>
7	bhz20wt	Indian white tiger	<i>Panthera tigris bengalensis</i>
8	bhz22wt	Indian white tiger	<i>Panthera tigris bengalensis</i>
9	bhz23wt	Indian white tiger	<i>Panthera tigris bengalensis</i>
10	bhz28wt	Indian white tiger	<i>Panthera tigris bengalensis</i>
11	gz1l	Normal leopard	<i>Panthera pardus</i>
12	gz2l	Normal leopard	<i>Panthera pardus</i>
13	gz3l	Normal leopard	<i>Panthera pardus</i>
14	gz21cl	Clouded leopard	<i>Neofelis nebulosa</i>
15	gz22cl	Clouded leopard	<i>Neofelis nebulosa</i>
16	darz14sl	Snow leopard	<i>Panthera uncia</i>
17	darz15sl	Snow leopard	<i>Panthera uncia</i>
18	darz16sl	Snow leopard	<i>Panthera uncia</i>
19	sbz22al	Asiatic lion	<i>Panthera leo persica</i>
20	sbz38al	Asiatic lion	<i>Panthera leo persica</i>
21	sbz39al	Asiatic lion	<i>Panthera leo persica</i>
22	humsk	Human	<i>Homo sapiens sapiens</i>
23	chimss	Chimpanzee	<i>Pan sp.</i>

Table 6. Multiple sequence alignments of the cytochrome b sequences of reference animals with the sequence obtained from confiscated animal remain

sbz22al	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	50
sbz38al	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
sbz39al	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
adil.flesh	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCTTGACACGATTCTTTGCCCTTCCAC	60
gz1nl	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCTTGACACGATTCTTTGCCCTTCCAC	60
gz2nl	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCTTGACACGATTCTTTGCCCTTCCAC	60
gz3nl	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCTTGACACGATTCTTTGCCCTTCCAC	60
bhz23wt	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
bhz28wt	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
bhz22wt	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
bhz20wt	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
bhz63t	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
bhz56t	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
bhz26t	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
bhz30t	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
bhz45t	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
bhz25t	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
d=14s1	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
d=15s1	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
d=16s1	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
gz21cl	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
gz22cl	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
chimss	TGAATCTGAGGAGGCTACTCAGTAGACAGCCCTACCCCTTACACGATTCTTTACCTTCCAC	60
humsk	TGAATCTGAGGAGGCTACTCAGTAGACAGTCCCACCCTCACACGATTCTTTACCTTCCAC	60
*****		
sbz22al	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCCTCCATGAA	120
sbz38al	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCCTCCATGAA	120
sbz39al	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCCTCCATGAA	120
adil.flesh	TTTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCCTCAGGAG	120
gz1nl	TTTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCCTCAGGAG	120
gz2nl	TTTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCCTCAGGAG	120
gz3nl	TTTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCCTCAGGAG	120
bhz23wt	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
bhz28wt	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
bhz22wt	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
bhz20wt	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
bhz63t	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
bhz56t	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
bhz26t	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
bhz30t	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
bhz45t	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
bhz25t	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
d=14s1	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
d=15s1	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
d=16s1	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
gz21cl	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
gz22cl	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
chimss	TTTATCTTACCTTTCATTATCAGAGCCCTAACCAACTTCATCTCCTATTCTTACACGAA	120
humsk	TTTCATCTTGCCCTTCATTATTGAGCCCTAGCAGCAGTCCACCTCCTATTCTTACACGAA	120
.. .. .		
sbz22al	ACAGGATCTAAATAACCCCTCAGGAATGGTATCTGACTCAGATAAAAATTCGATTCCATCCA	190
sbz38al	ACAGGATCTAAATAACCCCTCAGGAATGGTATCTGACTCAGATAAAAATTCGATTCCATCCA	190



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bh228wt      GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA 300
bh222wt      GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA 300
bh220wt      GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA 300
bh263t       GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA 300
bh256t       GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA 300
bh226t       GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA 300
bh230t       GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA 300
bh245t       GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA 300
bh225t       GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA 300
d214s1      GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA 300
d215s1      GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA 300
d216s1      GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA 300
g221c1      GTTCTATTCTCCCCAGACCTACTAGGAGACCCTGACAATTACACTCCCCGCCAACCCCTCTA 300
g222c1      GTTCTATTCTCCCCAGACCTACTAGGAGACCCTGACAATTACACTCCCCGCCAACCCCTCTA 300
chimss      ACACTATTCTCACCAGACCTCCTGGGCGATCCAGACAATTATACCCTAGCTAACCCCTTA 300
humsk       ACACTATTCTCACCAGACCTCCTAGGCGACCCAGACAATTATACCCTAGCCAAACCCCTTA 300

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sb222a1     AGCACCCCTCCCCATATCAAACCTGAAT 328
sb238a1     AGCACCCCTCCCCATATCAAACCTGAAT 328
sb239a1     AGCACCCCTCCCCATATCAAACCTGAAT 328
adil.flesh  AATACCCCTCCCCATATCAAGCCTGAAT 328
g21n1      AATACCCCTCCCCATATCAAGCCTGAAT 328
g22n1      AATACCCCTCCCCATATCAAGCCTGAAT 328
g23n1      AATACCCCTCCCCATATCAAGCCTGAAT 328
bh223wt     AACACCCCTCCCCATATCAAGCGCGAAT 328
bh228wt     AACACCCCTCCCCATATCAAGCGCGAAT 328
bh222wt     AACACCCCTCCCCATATCAAGCGCGAAT 328
bh220wt     AACACCCCTCCCCATATCAAGCGCGAAT 328
bh263t      AACACCCCTCCCCATATCAAGCGCGAAT 328
bh256t      AACACCCCTCCCCATATCAAGCGCGAAT 328
bh226t      AACACCCCTCCCCATATCAAGCGCGAAT 328
bh230t      AACACCCCTCCCCATATCAAGCGCGAAT 328
bh245t      AACACCCCTCCCCATATCAAGCGCGAAT 328
bh225t      AACACCCCTCCCCATATCAAGCGCGAAT 328
d214s1     AACACCCCTCCCCATATCAAGCCCGAAT 328
d215s1     AACACCCCTCCCCATATCAAGCCCGAAT 328
d216s1     AACACCCCTCCCCATATCAAGCCCGAAT 328
g221c1     AATACCCCTCCCCATATCAAGCCTGAAT 328
g222c1     AATACCCCTCCCCATATCAAGCCTGAAT 328
chimss     AACACCCCACCCCACATTAAACCCGAAT 328
humsk      AACACCCCTCCCCACATCAAGCCCGAAT 328

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\* \* \* \* \*











Table 8. Percent similarity matrix calculated by pair-wise comparisons of cytochrome b gene sequences revealed from 'adil.flesh' and different felids

	bhz20wt	bhz25t	dz14sl	humsk	chlmss	sbz22al	gz1L	gz2L	gz3L	gz21cl	adil.flesh
bhz20wt		100	99.1	81.7	78.7	93.3	95.1	95.4	95.4	89.6	95.4
bhz25t	100		99.1	81.7	78.7	93.3	95.1	95.4	95.4	89.6	95.4
dz14sl	99.1			81.4	78.4	93	94.8	95.1	95.1	89.3	95.1
humsk	81.7	81.7	81.4		86.9	79.6	81.1	80.2	80.2	79	81.4
chlmss	78.7	78.7	78.4	86.9		78.7	79.6	78.7	78.7	76.8	79.9
sbz22al	93.3	93.3	93	79.6	78.7		92.1	92.4	92.4	89	92.4
gz1L	95.1	95.1	94.8	81.1	79.6	92.1		98.5	98.5	89.3	99.7
gz2L	95.4	95.4	95.1	80.2	78.7	92.4	98.5		100	88.1	98.2
gz3L	95.4	95.4	95.1	80.2	78.7	92.4	98.5	100		88.1	98.2
gz21cl	89.6	89.6	89.3	79	76.8	89	89.3	88.1	88.1		89.6
adil.flesh	95.4	95.4	95.1	81.4	79.9	92.4	99.7	98.2	98.2	89.6	

## Table 10



BLASTN 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997). "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984591695-10075-13605

Query=

(25 letters)

Database: nt

807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reportsDistribution of 500 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



## Sequences producing significant alignments:

	Score (bits)	E Value
gb AF231651.1 AF231651 Strongylura notata clone HB-82 cyto...	50	2e-05
gb AF231650.1 AF231650 Strongylura notata clone HB-159 cyto...	50	2e-05
ref NC_002672.1  Dinornis giganteus mitochondrion, complete...	50	2e-05
ref NC_002673.1  Emeus crassus mitochondrion, complete genome	50	2e-05
gb AF232015.1 AF232015 Nothrotheriops shastensis cytochrome...	50	2e-05
gb AF232013.1 AF232013 Bradypus variegatus cytochrome b gen...	50	2e-05
gb AY016015.1  Emeus crassus mitochondrion, complete genome	50	2e-05
gb AY016013.1  Dinornis giganteus mitochondrion, complete g...	50	2e-05
gb AY016014.1  Dromaius novaehollandiae mitochondrion, part...	50	2e-05
gb AF230167.1 AF230167 Bonasa umbellus cytochrome b (CYTB) ...	50	2e-05
gb AF074594.1 AF074594 Baeolophus bicolor cytochrome b gene...	50	2e-05
gb AY005210.1  Poospiza melanoleuca isolate 3 cytochrome b ...	50	2e-05
gb AY005209.1  Poospiza melanoleuca isolate 2 cytochrome b ...	50	2e-05
gb AY005208.1  Poospiza melanoleuca isolate 1 cytochrome b ...	50	2e-05
gb AY005205.1  Poospiza hispaniolensis cytochrome b (cytb) ...	50	2e-05
gb AY005204.1  Poospiza garleppi cytochrome b (cytb) gene, ...	50	2e-05
gb AY005203.1  Poospiza erythrophrys cytochrome b (cytb) ge...	50	2e-05
gb AY005201.1  Poospiza boliviana cytochrome b (cytb) gene...	50	2e-05
gb AY005199.1  Poospiza alticola isolate 2 cytochrome b (cy...	50	2e-05
gb AY005198.1  Poospiza alticola isolate 1 cytochrome b (cy...	50	2e-05
gb AF155870.1 AF155870 Heterocephalus glaber cytochrome b (...)	50	2e-05
gb AF189123.1 AF189123 Glyptotermes eukalypti cytochrome b ...	50	2e-05
gb AF102099.1 AF102099 Criniferoides leucogaster cytochrome...	50	2e-05
gb AF102095.1 AF102095 Corythaixoides concolor cytochrome...	50	2e-05
gb AF271065.1 AF271065 Mustela erminea specimen-voucher AF1...	50	2e-05
gb AF243857.1 AF243857 Strongylura notata notata cytochrome...	50	2e-05
gb AF243856.1 AF243856 Strongylura notata forsythia cytochr...	50	2e-05
ref NC_001567.1  Bos taurus mitochondrion, complete genome	50	2e-05
gb AF306872.1 AF306872 Brachyramphus marmoratus haplotype M...	50	2e-05
gb AF306871.1 AF306871 Brachyramphus marmoratus haplotype M...	50	2e-05
gb AF306870.1 AF306870 Brachyramphus brevirostris haplotype...	50	2e-05
gb AF306869.1 AF306869 Brachyramphus brevirostris haplotype...	50	2e-05
gb AF306868.1 AF306868 Brachyramphus brevirostris haplotype...	50	2e-05
gb AF010406.1 AF010406 Ovis aries complete mitochondrial ge...	50	2e-05
gb AF248662.1 AF248662 Gryllus campestris haplotype 2 cyto...	50	2e-05
gb AF248661.1 AF248661 Gryllus campestris haplotype 1 cyto...	50	2e-05
gb AF096462.1 AF096462 Rhipidura albicollis cytochrome b ge...	50	2e-05
gb AF283644.1 AF283644 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283643.1 AF283643 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283642.1 AF283642 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283641.1 AF283641 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283640.1 AF283640 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283639.1 AF283639 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283637.1 AF283637 Elaphe obsoleta LSUMZ 45159 cytochro...	50	2e-05
gb AF283636.1 AF283636 Elaphe obsoleta LSUMZ 44662 cytochro...	50	2e-05
gb AF283635.1 AF283635 Elaphe obsoleta LSUMZ 40443 cytochro...	50	2e-05
gb AF283634.1 AF283634 Elaphe obsoleta LSUMZ 44335 cytochro...	50	2e-05
gb AF283633.1 AF283633 Elaphe obsoleta LSUMZ 42624 cytochro...	50	2e-05
gb AF283632.1 AF283632 Elaphe obsoleta LSUMZ H1911 cytochro...	50	2e-05
gb AF283631.1 AF283631 Elaphe obsoleta LSUMZ 41197 cytochro...	50	2e-05
gb AF283630.1 AF283630 Elaphe obsoleta LSUMZ 41189 cytochro...	50	2e-05
gb AF283629.1 AF283629 Elaphe obsoleta LSUMZ 41188 cytochro...	50	2e-05
gb AF283628.1 AF283628 Elaphe obsoleta LSUMZ 41187 cytochro...	50	2e-05
gb AF283627.1 AF283627 Elaphe obsoleta LSUMZ 41186 cytochro...	50	2e-05
gb AF283626.1 AF283626 Elaphe obsoleta LSUMZ 40943 cytochro...	50	2e-05
gb AF283625.1 AF283625 Elaphe obsoleta LSUMZ 37499 cytochro...	50	2e-05
gb AF283624.1 AF283624 Elaphe obsoleta LSUMZ 44480 cytochro...	50	2e-05
gb AF283623.1 AF283623 Elaphe obsoleta LSUMZ 44451 cytochro...	50	2e-05
gb AF283622.1 AF283622 Elaphe obsoleta LSUMZ 40444 cytochro...	50	2e-05
gb AF283621.1 AF283621 Elaphe obsoleta LSUMZ 37225 cytochro...	50	2e-05
gb AF283620.1 AF283620 Elaphe obsoleta LSUMZ 37163 cytochro...	50	2e-05
gb AF283619.1 AF283619 Elaphe obsoleta LSUMZ 37162 cytochrom...	50	2e-05
gb AF283618.1 AF283618 Elaphe obsoleta LSUMZ H15876 cytochr...	50	2e-05
gb AF283617.1 AF283617 Elaphe obsoleta LSUMZ H15872 cytochr...	50	2e-05
gb AF283616.1 AF283616 Elaphe obsoleta LSUMZ 15871 cytochro...	50	2e-05
gb AF283615.1 AF283615 Elaphe obsoleta LSUMZ H15870 cytochr...	50	2e-05
gb AF283614.1 AF283614 Elaphe obsoleta LSUMZ H15867 cytochr...	50	2e-05
gb AF283613.1 AF283613 Elaphe obsoleta LSUMZ H15864 cytochr...	50	2e-05

Table 9. Animals selected for validation of minimum P'S score for efficient amplification of DNA templates in PCR

SL.	Name	P, S/AFF	P, S/AFR
1	Indian black buck ( <i>Antelope cervicapra</i> )	97, 58	96, 54
2	Sheep ( <i>Ovis</i>	87, 53	96, 54
3	Pig ( <i>Sus scrofa</i> )	87, 52	87, 41
4	Fresh water dolphin ( <i>Platanista gangetica</i> )	86, 49	82, 47

## Sequences producing significant alignments:

	Score (bits)	E Value
gb AF231651.1 AF231651 Strongylura notata clone HB-82 cyto...	50	2e-05
gb AF231650.1 AF231650 Strongylura notata clone HB-159 cyto...	50	2e-05
ref NC_002672.1  Dinornis giganteus mitochondrion, complete...	50	2e-05
ref NC_002673.1  Emeus crassus mitochondrion, complete genome	50	2e-05
gb AF232015.1 AF232015 Nothrotheriops shastensis cytochrome...	50	2e-05
gb AF232013.1 AF232013 Bradypus variegatus cytochrome b gen...	50	2e-05
gb AY016015.1  Emeus crassus mitochondrion, complete genome	50	2e-05
gb AY016013.1  Dinornis giganteus mitochondrion, complete g...	50	2e-05
gb AY016014.1  Dromaius novaehollandiae mitochondrion, part...	50	2e-05
gb AF230167.1 AF230167 Bonasa umbellus cytochrome b (CYTB) ...	50	2e-05
gb AF074594.1 AF074594 Baolophus bicolor cytochrome b gene...	50	2e-05
gb AY005210.1  Poospiza melanoleuca isolate 3 cytochrome b ...	50	2e-05
gb AY005209.1  Poospiza melanoleuca isolate 2 cytochrome b ...	50	2e-05
gb AY005208.1  Poospiza melanoleuca isolate 1 cytochrome b ...	50	2e-05
gb AY005205.1  Poospiza hispaniolensis cytochrome b (cytb) ...	50	2e-05
gb AY005204.1  Poospiza garleppi cytochrome b (cytb) gene, ...	50	2e-05
gb AY005203.1  Poospiza erythrophrys cytochrome b (cytb) ge...	50	2e-05
gb AY005201.1  Poospiza boliviana cytochrome b (cytb) gene,...	50	2e-05
gb AY005199.1  Poospiza alticola isolate 2 cytochrome b (cy...	50	2e-05
gb AY005198.1  Poospiza alticola isolate 1 cytochrome b (cy...	50	2e-05
gb AF155870.1 AF155870 Heterocephalus glaber cytochrome b (...)	50	2e-05
gb AF189123.1 AF189123 Glyptotermes eukalypti cytochrome b ...	50	2e-05
gb AF102099.1 AF102099 Criniferoides leucogaster cytochrome...	50	2e-05
gb AF102095.1 AF102095 Corythaixoides concolor cytochrome...	50	2e-05
gb AF271065.1 AF271065 Mustela erminea specimen-voucher AF1...	50	2e-05
gb AF243857.1 AF243857 Strongylura notata notata cytochrome...	50	2e-05
gb AF243856.1 AF243856 Strongylura notata forsythia cytochr...	50	2e-05
ref NC_001567.1  Bos taurus mitochondrion, complete genome	50	2e-05
gb AF306872.1 AF306872 Brachyramphus marmoratus haplotype M...	50	2e-05
gb AF306871.1 AF306871 Brachyramphus marmoratus haplotype M...	50	2e-05
gb AF306870.1 AF306870 Brachyramphus brevirostris haplotype...	50	2e-05
gb AF306869.1 AF306869 Brachyramphus brevirostris haplotype...	50	2e-05
gb AF306868.1 AF306868 Brachyramphus brevirostris haplotype...	50	2e-05
gb AF010406.1 AF010406 Ovis aries complete mitochondrial ge...	50	2e-05
gb AF248662.1 AF248662 Gryllus campestris haplotype 2 cyto...	50	2e-05
gb AF248661.1 AF248661 Gryllus campestris haplotype 1 cyto...	50	2e-05
gb AF096462.1 AF096462 Rhipidura albicollis cytochrome b ge...	50	2e-05
gb AF283644.1 AF283644 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283643.1 AF283643 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283642.1 AF283642 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283641.1 AF283641 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283640.1 AF283640 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283639.1 AF283639 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283637.1 AF283637 Elaphe obsoleta LSUMZ 45359 cytochro...	50	2e-05
gb AF283636.1 AF283636 Elaphe obsoleta LSUMZ 44662 cytochro...	50	2e-05
gb AF283635.1 AF283635 Elaphe obsoleta LSUMZ 40443 cytochro...	50	2e-05
gb AF283634.1 AF283634 Elaphe obsoleta LSUMZ 44335 cytochro...	50	2e-05
gb AF283633.1 AF283633 Elaphe obsoleta LSUMZ 42624 cytochro...	50	2e-05
gb AF283632.1 AF283632 Elaphe obsoleta LSUMZ H1911 cytochro...	50	2e-05
gb AF283631.1 AF283631 Elaphe obsoleta LSUMZ 41197 cytochro...	50	2e-05
gb AF283630.1 AF283630 Elaphe obsoleta LSUMZ 41189 cytochro...	50	2e-05
gb AF283629.1 AF283629 Elaphe obsoleta LSUMZ 41188 cytochro...	50	2e-05
gb AF283628.1 AF283628 Elaphe obsoleta LSUMZ 41187 cytochro...	50	2e-05
gb AF283627.1 AF283627 Elaphe obsoleta LSUMZ 41186 cytochro...	50	2e-05
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gb AF283625.1 AF283625 Elaphe obsoleta LSUMZ 37499 cytochro...	50	2e-05
gb AF283624.1 AF283624 Elaphe obsoleta LSUMZ 44480 cytochro...	50	2e-05
gb AF283623.1 AF283623 Elaphe obsoleta LSUMZ 44451 cytochro...	50	2e-05
gb AF283622.1 AF283622 Elaphe obsoleta LSUMZ 40444 cytochro...	50	2e-05
gb AF283621.1 AF283621 Elaphe obsoleta LSUMZ 37725 cytochro...	50	2e-05
gb AF283620.1 AF283620 Elaphe obsoleta LSUMZ 37163 cytochro...	50	2e-05
gb AF283619.1 AF283619 Elaphe obsoleta LSUMZ 37162 cytochrom...	50	2e-05
gb AF283618.1 AF283618 Elaphe obsoleta LSUMZ H15876 cytochr...	50	2e-05
gb AF283617.1 AF283617 Elaphe obsoleta LSUMZ H15872 cytochr...	50	2e-05
gb AF283616.1 AF283616 Elaphe obsoleta LSUMZ 15871 cytochro...	50	2e-05
gb AF283615.1 AF283615 Elaphe obsoleta LSUMZ H15870 cytochr...	50	2e-05
gb AF283614.1 AF283614 Elaphe obsoleta LSUMZ H15867 cytochr...	50	2e-05
gb AF283613.1 AF283613 Elaphe obsoleta LSUMZ H15866 cytochr...	50	2e-05



gb AF283612.1 AF283612	Elaphe obsoleta LSUMZ H15884 cytochr...	50	2e-05
gb AF283611.1 AF283611	Elaphe obsoleta LSUMZ H15031 cytochr...	50	2e-05
gb AF283610.1 AF283610	Elaphe obsoleta LSUMZ H15030 cytochr...	50	2e-05
gb AF283609.1 AF283609	Elaphe obsoleta CAS 169468 cytochrom...	50	2e-05
gb AF283608.1 AF283608	Elaphe obsoleta LSUMZ H14782 cytochr...	50	2e-05
gb AF283607.1 AF283607	Elaphe obsoleta LSUMZ H14781 cytochr...	50	2e-05
gb AF283606.1 AF283606	Elaphe obsoleta LSUMZ H14724 cytochr...	50	2e-05
gb AF283605.1 AF283605	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283604.1 AF283604	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283603.1 AF283603	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283602.1 AF283602	Elaphe obsoleta LSUMZ H3388 cytochro...	50	2e-05
gb AF283601.1 AF283601	Elaphe obsoleta LSUMZ H3385 cytochro...	50	2e-05
gb AF283600.1 AF283600	Elaphe obsoleta LSUMZ H3384 cytochro...	50	2e-05
gb AF283599.1 AF283599	Elaphe bairdi LSUMZ H3382 cytochrome...	50	2e-05
gb AF283598.1 AF283598	Elaphe bairdi LSUMZ H3381 cytochrome...	50	2e-05
gb AF283597.1 AF283597	Elaphe obsoleta LSUMZ H3379 cytochro...	50	2e-05
gb AF283596.1 AF283596	Elaphe obsoleta LSUMZ 39616 cytochro...	50	2e-05
gb AF283595.1 AF283595	Elaphe obsoleta LSUMZ H3376 cytochro...	50	2e-05
gb AF283594.1 AF283594	Elaphe obsoleta LSUMZ H3345 cytochro...	50	2e-05
gb AF283593.1 AF283593	Elaphe obsoleta LSUMZ H3309 cytochro...	50	2e-05
gb AF283592.1 AF283592	Elaphe obsoleta LSUMZ H3306 cytochro...	50	2e-05
gb AF283591.1 AF283591	Elaphe obsoleta LSUMZ H3276 cytochro...	50	2e-05
gb AF283590.1 AF283590	Elaphe obsoleta LSUMZ H3246 cytochro...	50	2e-05
gb AF283589.1 AF283589	Elaphe obsoleta LSUMZ H3212 cytochro...	50	2e-05
gb AF283588.1 AF283588	Elaphe obsoleta LSUMZ H3209 cytochro...	50	2e-05
gb AF283587.1 AF283587	Elaphe obsoleta LSUMZ H3206 cytochro...	50	2e-05
gb AF283586.1 AF283586	Elaphe obsoleta LSUMZ H3191 cytochro...	50	2e-05
gb AF283585.1 AF283585	Elaphe obsoleta LSUMZ H3190 cytochro...	50	2e-05
gb AF283584.1 AF283584	Elaphe obsoleta LSUMZ H3189 cytochro...	50	2e-05
gb AF283583.1 AF283583	Elaphe obsoleta LSUMZ H3188 cytochro...	50	2e-05
gb AF283582.1 AF283582	Elaphe obsoleta LSUMZ H3186 cytochro...	50	2e-05
gb AF283581.1 AF283581	Elaphe obsoleta LSUMZ H3169 cytochro...	50	2e-05
gb AF283580.1 AF283580	Elaphe obsoleta CAS 203083 cytochrom...	50	2e-05
gb AF283579.1 AF283579	Elaphe obsoleta CAS 203079 cytochrom...	50	2e-05
gb AF283578.1 AF283578	Elaphe obsoleta LSUMZ H2286 cytochro...	50	2e-05
gb AF283577.1 AF283577	Elaphe obsoleta CAS 208631 cytochrom...	50	2e-05
gb AF283576.1 AF283576	Elaphe obsoleta LSUMZ H2229 cytochro...	50	2e-05
gb AF187030.1 AF187030	Rhinophylla pumilio isolate TK46001 ...	50	2e-05
gb AF310052.1 AF310052	Poospiza hispaniolensis cytochrome b...	50	2e-05
gb AF310046.1 AF310046	Volatinia jacarina cytochrome b gene...	50	2e-05
gb AF171919.1 AF171919	Deinagkistrodon acutus cytochrome b ...	50	2e-05
gb AF171897.1 AF171897	Trimeresurus mucrosquamatus cytb gen...	50	2e-05
gb AF290174.1 AF290174	Agelaius cyanopus cytochrome b (cytb...	50	2e-05
gb AF290173.1 AF290173	Agelaius phoeniceus cytochrome b (cy...	50	2e-05
gb AF290171.1 AF290171	Quiscalus major cytochrome b (cytb) ...	50	2e-05
gb AF290170.1 AF290170	Amblycercus holosericeus cytochrome ...	50	2e-05
gb AF290150.1 AF290150	Volatinia jacarina cytochrome b (cyc...	50	2e-05
gb AF176252.1 AF176252	Reithrodontomys zacatecae cytochrome...	50	2e-05
gb AF176251.1 AF176251	Reithrodontomys zacatecae cytochrome...	50	2e-05
gb AF163907.1 AF163907	Microtus xanthognathus cytochrome b ...	50	2e-05
gb AF163904.1 AF163904	Microtus pinetorum cytochrome b gene...	50	2e-05
gb AF163901.1 AF163901	Microtus ochrogaster cytochrome b ge...	50	2e-05
gb AF163899.1 AF163899	Microtus mivatus cytochrome b gene, c...	50	2e-05
gb AF163891.1 AF163891	Microtus californicus cytochrome B (...)	50	2e-05
gb AF163890.1 AF163890	Microtus abbreviatus cytochrome B (c...	50	2e-05
gb AF288524.1 AF288524	Dipsochelys dussumieri isolate Germa...	50	2e-05
gb AF288523.1 AF288523	Dipsochelys dussumieri isolate white...	50	2e-05
gb AF288522.1 AF288522	Dipsochelys dussumieri isolate Aldy ...	50	2e-05
gb AF123530.1 AF123530	Psilopogon pyrolophus cytochrome b (...)	50	2e-05
gb AF123512.1 AF123512	Eubucco bourcierii cucinkaе cytochro...	50	2e-05
gb AF206548.1 AF206548	Adolfus vauereselli cytochrome b gen...	50	2e-05
gb AF197857.1 AF197857	Gymnorhina tibicen cytochrome b gene...	50	2e-05
gb U63397.2 SEU63397	Sitta europaea cytochrome b gene, part...	50	2e-05
NC 001945.1	Dinodon semicarinatus mitochondrion, compl...	50	2e-05
NC 001821.1	Dasypus novemcinctus mitochondrion, comple...	50	2e-05
gb AF141217.1 AF141217	Dasymys incommis country Tanzania cy...	50	2e-05
gb AF201615.1 AF201615	Pantodon buchholzi cytochrome b gene...	50	2e-05
gb AF077920.1 AF077920	Bombus nevadensis cytochrome b gene...	50	2e-05
gb AF190612.1 AF190612	Oreamnos americanus cytochrome b (cy...	50	2e-05
gb J01124.1 BOVM	taurus mitochondrion, complete genome	50	2e-05
gb AF191810.1 AF191810	Cochlearius cochlearius cytochrome b...	50	2e-05

gb U89181.1 CAU89181	Chlorostilbon aureoventris cytochrome ...	50	2e-05
gb U89171.1 AFU89171	Asio flammeus cytochrome b (cytb) gene...	50	2e-05
gb AF217833.1 AF217833	Homoroselaps lacteus cytochrome b ge...	50	2e-05
gb AF217822.1 AF217822	Hydrophis semperi cytochrome b gene,...	50	2e-05
gb AF217813.1 AF217813	Acanthophis antarcticus cytochrome b...	50	2e-05
gb AF220408.1 AF220408	Calliophis kelloggi cytochrome b (cy...	50	2e-05
gb AF126430.1 AF126430	Ellobius fuscocapillus cytochrome b ...	50	2e-05
gb AF090337.1 AF090337	Aythya americana mitochondrion, comp...	50	2e-05
gb AF059111.1 AF059111	Sarkidiornis melanotos cytochrome b ...	50	2e-05
gb AF059053.1 AF059053	Aix sponsa cytochrome b gene, partia...	50	2e-05
gb AF099308.1 AF099308	Icterus wagleri wagleri cytochrome b...	50	2e-05
gb AF099295.1 AF099295	Icterus gularis yucatanensis cytochr...	50	2e-05
gb AF099294.1 AF099294	Icterus gularis tamaulipensis cytoch...	50	2e-05
gb AF099293.1 AF099293	Icterus gularis gularis cytochrome b...	50	2e-05
gb AF160610.1 AF160610	Cricetomys emini Cemi636 cytochrome ...	50	2e-05
gb AF036280.1 AF036280	Tragelaphus strepsiceros cytochrome ...	50	2e-05
gb AF036277.1 AF036277	Tragelaphus scriptus cytochrome b (c...	50	2e-05
gb AF036274.1	Tetracerus quadricornis cytochrome b (cytb) ...	50	2e-05
gb AF194218.1 AF194218	Phrynosoma platyrhinos cytochrome b ...	50	2e-05
gb AF194216.1 AF194216	Urosaurus ornatus cytochrome b gene,...	50	2e-05
ref NC_002009.1	Artibeus jamaicensis mitochondrion, comple...	50	2e-05
ref NC_001941.1	Ovis aries mitochondrion, complete genome	50	2e-05
ref NC_000877.1	Aythya americana mitochondrion, complete g...	50	2e-05
ref NC_000845.1	Rhea americana mitochondrion, complete genome	50	2e-05
gb U27551.1 GCU27551	Grus canadensis tabida cytochrome b (c...	50	2e-05
gb AF089058.1 AF089058	Quiscalus quiscula cytochrome b (cyt...	50	2e-05
gb AF089055.1 AF089055	Quiscalus major cytochrome b (cytb) ...	50	2e-05
gb AF089054.1 AF089054	Quiscalus lugubris cytochrome b (cyt...	50	2e-05
gb AF089046.1 AF089046	Oreopsar bolivianus cytochrome b (cy...	50	2e-05
gb AF089042.1 AF089042	Molothrus badius cytochrome b (cytb)...	50	2e-05
gb AF089039.1 AF089039	Macroagelaius imthurni cytochrome b ...	50	2e-05
gb AF089037.1 AF089037	Lamprosax tanagra cytochrome b (...	50	2e-05
gb AF089026.1 AF089026	Gymnomystax mexicanus cytochrome b (...	50	2e-05
gb AF089025.1 AF089025	Gnorimopsar chopi cytochrome b (cytb...	50	2e-05
gb AF089024.1 AF089024	Euphagus cyanocephalus cytochrome b ...	50	2e-05
gb AF089023.1 AF089023	Euphagus carolinus cytochrome b (cyt...	50	2e-05
gb AF089021.1 AF089021	Dives warstewiczi cytochrome b (cyt...	50	2e-05
gb AF089020.1 AF089020	Curaeus curaeus cytochrome b (cytb) ...	50	2e-05
gb AF089016.1 AF089016	Amblycercus holosericeus cytochrome ...	50	2e-05
gb AF089013.1 AF089013	Agelaius xanthophthalmus cytochrome ...	50	2e-05
gb AF089012.1 AF089012	Agelaius xanthomus cytochrome b (cyt...	50	2e-05
gb AF089008.1 AF089008	Agelaius phoeniceus sub-species phoe...	50	2e-05
gb AF089006.1 AF089006	Agelaius humeralis cytochrome b (cyt...	50	2e-05
gb AF089005.1 AF089005	Agelaius cyanopus cytochrome b (cytb...	50	2e-05
gb AF108695.1 AF108695	Scolomys jruaense cytochrome B (cyt...	50	2e-05
gb AF108685.1 AF108685	Wiedomys pyrrhorhinos cytochrome B (...	50	2e-05
gb AF108677.1 AF108677	Thomasomys oreas cytochrome B (cytB)...	50	2e-05
gb AF145511.1 AF145511	Melanoplus foedus cytochrome b gene,...	50	2e-05
gb AF145511.1 AF145511	Melanoplus angustipennis cytochrome ...	50	2e-05
gb U89627.1 BMU89627	Bolitoglossa marmorea cytochrome b (cy...	50	2e-05
gb U89623.1 BPU89623	Batrachoseps pacificus cytochrome b (c...	50	2e-05
gb AF181470.1 AF181470	Okapia johnstoni cytochrome b gene, ...	50	2e-05
gb AF084075.1 AF084075	Lagenorhynchus acutus cytochrome b g...	50	2e-05
gb U90303.1 OMU90303	Ovibos moschatus cytochrome b (cytb) g...	50	2e-05
gb U90302.1 OMU90302	Ovibos moschatus cytochrome b (cytb) g...	50	2e-05
gb U90301.1 OMU90301	Ovibos moschatus cytochrome b (cytb) g...	50	2e-05
gb U90300.1 OMU90300	Ovibos moschatus cytochrome b (cytb) g...	50	2e-05
gb AF038883.1 AF038883	Deinagkistrodon acutus cytochrome b ...	50	2e-05
gb AF039269.1 AF039269	Agkistrodon concolor cytochrome b ...	50	2e-05
gb AF039267.1 AF039267	Boa constrictor cytochrome b (cytb) ...	50	2e-05
gb S49215.1 S49215	apocytochrome b (sheep, domestic, Marino...	50	2e-05
gb AF158698.1 AF158698	Geomys pinetis cytochrome b gene, co...	50	2e-05
gb AF158692.1 AF158692	Geomys bursarius jugoslavicus cyto...	50	2e-05
gb AF058123.1 AF058123	Ichaginia cruentus cytochrome b (cyt...	50	2e-05
gb AF021629.1 AF021629	Antilocapra americana cytochrome b (...	50	2e-05
gb AF022063.1	Tragelaphus strepsiceros cytochrome b (cytb)...	50	2e-05
gb AF022062.1	Tragelaphus derbianus cytochrome b (cytb) ge...	50	2e-05
gb AF022060.1	Hippocragus equinus cytochrome b (cytb) gene...	50	2e-05
gb AF022057.1	Tragelaphus oryx cytochrome b (cytb) gene, m...	50	2e-05
gb AF111500.1 AF111500	Lagenorhynchus acutus isolate LACU74...	50	2e-05
gb AF111499.1 AF111499	Lagenorhynchus acutus isolate LACU73...	50	2e-05

gb U69644.1 EBU69644	Lexocemus bicolor cytochrome b (cytb) ...	50	2e-05
gb U69646.1 EBU69646	Eunectes notaeus cytochrome b (cytb) g...	50	2e-05
gb U69648.1 EBU69648	Eunectes murinus cytochrome b (cytb) g...	50	2e-05
gb U69799.1 ESU69799	Epicrates striatus fosteri cytochrome ...	50	2e-05
gb U69796.1 ESU69796	Epicrates striatus strigilatus cytochr...	50	2e-05
gb U69795.1 ESU69795	Epicrates striatus strigilatus cytochr...	50	2e-05
gb U69794.1 ESU69794	Epicrates striatus mcrauniei cytochrom...	50	2e-05
gb U69793.1 ESU69793	Epicrates striatus mcrauniei cytochrom...	50	2e-05
gb U69792.1 EMU69792	Epicrates monensis cytochrome b (cytb)...	50	2e-05
gb U69790.1 EMU69790	Epicrates monensis cytochrome b (cytb)...	50	2e-05
gb U69786.1 EFU69786	Epicrates fordi cytochrome b (cytb) ge...	50	2e-05
gb U69784.1 EFU69784	Epicrates fordi cytochrome b (cytb) ge...	50	2e-05
gb U69779.1 ECU69779	Epicrates cenchria cytochrome b (cytb)...	50	2e-05
gb U69777.1 ECU69777	Epicrates cenchria cytochrome b (cytb)...	50	2e-05
gb U69776.1 EAU69776	Epicrates angulifer cytochrome b (cytb)...	50	2e-05
gb U69774.1 EAU69774	Epicrates angulifer cytochrome b (cytb)...	50	2e-05
gb U69772.1 CEU69772	Corallus enydris cytochrome b (cytb) g...	50	2e-05
gb U69771.1 CEU69771	Corallus enydris cytochrome b (cytb) g...	50	2e-05
gb U69770.1 CEU69770	Corallus enydris cytochrome b (cytb) g...	50	2e-05
gb U69769.1 CEU69769	Corallus enydris cytochrome b (cytb) g...	50	2e-05
gb U69752.1 CAU69752	Candoia aspera cytochrome b (cytb) gen...	50	2e-05
gb U69746.1 BCU69746	Boa constrictor cytochrome b (cytb) ge...	50	2e-05
gb U69740.1 BCU69740	Boa constrictor cytochrome b (cytb) ge...	50	2e-05
gb AF139057.1 AF139057	Isodon macrourus cytochrome b gene,...	50	2e-05
gb AF090339.1 AF090339	Rhea americana mitochondrion, comple...	50	2e-05
gb AF006275.1 AF006275	Cnemidophorus tigris strain Isla Ang...	50	2e-05
gb AF006267.1 AF006267	Cnemidophorus tigris strain Isla Smi...	50	2e-05
gb AF034969.1 AF034969	Connochaetes taurinus cytochrome b g...	50	2e-05
gb AF028822.1 AF028822	Alcelaphus buselaphus cytochrome b g...	50	2e-05
gb AF028821.1 AF028821	Damaliscus lunatus cytochrome b gene...	50	2e-05
gb AF061340.1 AF061340	Artibeus jamaicensis mitochondrial D...	50	2e-05
gb AF076093.1 AF076093	Thalassarche impavida cytochrome b (...)	50	2e-05
gb AF076091.1 AF076091	Thalassarche carteri cytochrome b (c...	50	2e-05
gb AF076072.1 AF076072	Pelagodroma marina cytochrome b (cyt...	50	2e-05
gb AF076063.1 AF076063	Oceanodroma furcata cytochrome b (cy...	50	2e-05
gb AF076059.1 AF076059	Hydrobates pelagicus cytochrome b (c...	50	2e-05
gb AF076056.1 AF076056	Garrodia nareis cytochrome b (cytb) ...	50	2e-05
gb AF076053.1 AF076053	Fregatta tropica cytochrome b (cytb)...	50	2e-05
gb AF076050.1 AF076050	Diomedea gibsoni cytochrome b (cytb)...	50	2e-05
gb AF076049.1 AF076049	Diomedea epomophora cytochrome b (cy...	50	2e-05
gb AF076048.1 AF076048	Diomedea chionoptera cytochrome b (c...	50	2e-05
gb AF076047.1 AF076047	Diomedea antipodensis cytochrome b (...)	50	2e-05
gb U83314.1 MSU83314	Microstus semitorquatus cytochrome b (...)	50	2e-05
gb U83318.1 MEU83318	Microhierax erythrogenys cytochrome b ...	50	2e-05
gb U37303.1 SAU37303	Synthliboramphus antiquus cytochrome b...	50	2e-05
gb U37302.1 PAU37302	Ptychoramphus aleuticus cytochrome b g...	50	2e-05
gb U37296.1 CPU37296	Cyclorhynchus psittacula cytochrome b...	50	2e-05
gb U37289.1 BBU37289	Brachyramphus brevirostris cytochrome ...	50	2e-05
gb U37286.1 APU37286	Aethia pygmaea cytochrome b gene, mito...	50	2e-05
gb U37104.1 APU37104	Aethia pusilla cytochrome b gene, mito...	50	2e-05
gb U37087.1 ACU37087	Aethia cristatella cytochrome b gene, ...	50	2e-05
gb U87525.1 HGU87525	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb U87524.1 HGU87524	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb U87523.1 HGU87523	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb U87522.1 HGU87522	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb U17864.1 STU17864	Saiga tatarica cytochrome b gene, mito...	50	2e-05
gb U17861.1 QAU17861	Oreamnos americanus cytochrome b gene...	50	2e-05
gb U17862.1 OMU17862	Ovibos moschatus moschatus cytochrome ...	50	2e-05
gb U17860.1 ODU17860	Ovis dalli cytochrome b gene, mitochon...	50	2e-05
gb U17859.1 OCU17859	Ovis canadensis cytochrome b gene, mit...	50	2e-05
gb U65274.1 TBU65274	Thomomys bottae cytochrome b (cytb) ge...	50	2e-05
gb U65267.1 TBU65267	Thomomys bottae cytochrome b (cytb) ge...	50	2e-05
gb U65260.1 TBU65260	Thomomys bottae cytochrome b (cytb) ge...	50	2e-05
gb U65101.1 PAU65101	Perognathus amplius cytochrome b (cytb)...	50	2e-05
gb AF034739.1 AF034739	Capra aegagrus cytochrome b (cytb) g...	50	2e-05
gb AF034738.1 AF034738	Capra caucasica cytochrome b (cytb) gene, mito...	50	2e-05
gb AF034737.1 AF034737	Capra cylindricornis cytochrome b (cytb) gen...	50	2e-05
gb AF034736.1 AF034736	Capra falconeri cytochrome b (cytb) ...	50	2e-05
gb AF034735.1 AF034735	Capra ibex cytochrome b (cytb) gene, mitoch...	50	2e-05
gb AF034730.1 AF034730	Ovis arles cytochrome b (cytb) gene, ...	50	2e-05
gb AF034722.1 AF034722	Ovis vignei cytochrome b (cytb) gene...	50	2e-05

gb AF034724.1	Ovis dalli dalli cytochrome b (cytb) gene, m...	50	2e-05
gb AF034727.1	Ovis ammon darwini cytochrome b (cytb) gene...	50	2e-05
gb AF034724.1 AF034724	Pantholops hodgsoni cytochrome b (cy...	50	2e-05
gb AF057132.1 AF057132	Taxidea taxus cytochrome b (cytb) ge...	50	2e-05
gb U94805.1 TMU94805	Trogon melanurus cytochrome b gene, mi...	50	2e-05
gb U94804.1 TCU94804	Trogon comptus cytochrome b gene, mito...	50	2e-05
gb U94803.1 TVU94803	Trogon viridis cytochrome b gene, mito...	50	2e-05
gb AF006251.1 AF006251	Sericossypha albocristata cytochrome...	50	2e-05
gb AF006249.1 AF006249	Pyrrhocoma ruficeps cytochrome b (cy...	50	2e-05
gb AF006238.1 AF006238	Lamprospiza melanoleuca cytochrome b...	50	2e-05
gb AF006234.1 AF006234	Hemispingus acropileus cytochrome b ...	50	2e-05
gb AF006226.1 AF006226	Cypsnagra hirundinacea cytochrome b ...	50	2e-05
gb AF006215.1 AF006215	Chlorophanes spiza cytochrome b (cyt...	50	2e-05
gb AF006214.1 AF006214	Chlorochrysa calliparaea cytochrome ...	50	2e-05
gb AF006213.1 AF006213	Calochaetes coccineus cytochrome b (...)	50	2e-05
gb AF006212.1 AF006212	Buthraupis montana cytochrome b (cyt...	50	2e-05
emb AJ293419.1 RRU293419	Rupicapra rupicapra rupicapra mito...	50	2e-05
emb AJ293416.1 RPY293416	Rupicapra pyrenaica pyrenaica mito...	50	2e-05
emb AJ293415.1 RPY293415	Rupicapra pyrenaica parva mitochon...	50	2e-05
emb AJ293414.1 RPY293414	Rupicapra pyrenaica ornata mitochon...	50	2e-05
emb AJ293412.1 RRU293412	Rupicapra rupicapra rupicapra mito...	50	2e-05
emb AJ293418.1 CFA293418	Capra falconeri mitochondrial part...	50	2e-05
gb U07578.1 DCU07578	Dasycercus cristicauda mitochondrion c...	50	2e-05
emb AJ004180.1 HPAJ4180	Hydrobates pelagicus mitochondrial ...	50	2e-05
emb Y15695.1 SMY15695	Schilbe mystus mitochondrial cytb gen...	50	2e-05
emb Y15697.1 EDY15697	Eutropius depressirostris mitochondri...	50	2e-05
emb Y15696.1 EDY15696	Eutropius depressirostris mitochondri...	50	2e-05
gb AF015035.1 AF015035	Steatocranus casuarinus 20 cytochrom...	50	2e-05
gb AF015761.1 AF015761	Palmeria dolei cytochrome b (Cytb) g...	50	2e-05
gb AF015758.1 AF015758	Oreomystis mana cytochrome b (Cytb) ...	50	2e-05
gb AF015756.1 AF015756	Vestiaria coccinea cytochrome b (Cyt...	50	2e-05
gb AF015754.1 AF015754	Himatione sanguinea cytochrome b (Cy...	50	2e-05
gb U76052.1 DNU76052	Dromaius novaehollandiae cytochrome b ...	50	2e-05
emb AJ236634.1 CGL236634	Clethrionomys glareolus mitochondr...	50	2e-05
gb U83158.1 POU83158	Pelecanus onocrotalus cytochrome B gen...	50	2e-05
gb U83157.1 POU83157	Pelecanus onocrotalus cytochrome B gen...	50	2e-05
gb U83156.1 AAU83156	Anhinga anhinga cytochrome B gene, mit...	50	2e-05
gb U83155.1 AAU83155	Anhinga anhinga cytochrome B gene, mit...	50	2e-05
gb U83154.1 AAU83154	Anhinga anhinga cytochrome B gene, mit...	50	2e-05
gb U83156.1 CLU83156	Chelodina longicollis cytochrome b gen...	50	2e-05
emb AJ277676.1 ESC277676	Elaphe scalaris mitochondrial part...	50	2e-05
emb AJ277675.1 ESC277675	Elaphe scalaris mitochondrial part...	50	2e-05
emb AJ277672.1 ELO277672	Elaphe longissima mitochondrial pa...	50	2e-05
emb AJ277671.1 ELO277671	Elaphe longissima mitochondrial pa...	50	2e-05
emb Y11832.1 MTNCOMGN	Dasypus novemcinctus complete mitoch...	50	2e-05
emb AJ388467.1 NBA388467	Nemacheilus barbatulus mitochondria...	50	2e-05
emb AJ388468.1 IME388468	Ictalurus melas mitochondrial cyt b...	50	2e-05
emb AJ388459.1 LDE388459	Leucaspius delineatus mitochondrial...	50	2e-05
gb U46167.1 SCU46167	Sciurus carolinensis cytochrome b gene...	50	2e-05
emb AJ245673.1 SIN245673	Schilbe intermedius partial mitoch...	50	2e-05
emb AJ245638.1 SIN245638	Schilbe intermedius partial mitoch...	50	2e-05
emb AJ245678.1 EDE245678	Eutropius depressirostris partial ...	50	2e-05
emb AJ245677.1 EDE245677	Eutropius depressirostris partial ...	50	2e-05
emb AJ245676.1 EDE245676	Eutropius depressirostris partial ...	50	2e-05
emb AJ245675.1 EDE245675	Eutropius depressirostris partial ...	50	2e-05
emb AJ245674.1 EDE245674	Eutropius depressirostris partial ...	50	2e-05
emb Y15884.1 MTRACOMPL	Rhea americana complete mitochondria...	50	2e-05
gb U60768.1 PCU60768	Parus cinctus cytochrome b gene, mitoc...	50	2e-05
gb U48955.1 TMU48955	Thalassarche melanophris melanophris c...	50	2e-05
gb U48954.1 TCU48954	Thalassarche chrysostoma cytochrome b ...	50	2e-05
gb U48944.1 TCU48944	Thalassarche chlorochymos chlorochym...	50	2e-05
gb U48943.1 PPU48943	Phoebastria palpebrata cytochrome b (cy...	50	2e-05
gb U48942.1 PFU48942	Phoebastria fusca cytochrome b (cytb) g...	50	2e-05
gb U48941.1 MCU48941	Macronectes giganteus cytochrome b (cy...	50	2e-05
gb U48947.1 DEU48947	Diomedea exulans dabbenena cytochrome ...	50	2e-05
gb U48946.1 DEU48946	Diomedea epomophora sanfordi cytochrom...	50	2e-05
gb U48949.1 PAU48949	Diomedea amsterdamsis cytochrome b (...)	50	2e-05
gb U55725.1 PRU55725	Piranga rubra cytochrome b gene, mitoc...	50	2e-05
gb U55509.1 APU55509	Artibeus planirostris cytochrome b (cy...	50	2e-05
gb U55507.1 AQU55507	Artibeus obscurus cytochrome b (cytb) ...	50	2e-05
gb U55505.1 AQU55505	Artibeus obscurus cytochrome b (cytb) ...	50	2e-05

gb U66505.1 ALUG6505	Artibeus lituratus cytochrome b (cytb)...	50	2e-05
gb U66504.1 AJU66504	Artibeus jamaicensis cytochrome b (cyt...	50	2e-05
gb U66503.1 AJU66503	Artibeus jamaicensis cytochrome b (cyt...	50	2e-05
gb U66502.1 AIU66502	Artibeus intermedius cytochrome b (cyt...	50	2e-05
gb U66501.1 AZU66501	Artibeus inopinatus cytochrome b (cytb...	50	2e-05
gb U66500.1 AHU66500	Artibeus hirsutus cytochrome b (cytb)	50	2e-05
gb U66499.1 AFU66499	Artibeus fraterculus cytochrome b (cyt...	50	2e-05
gb U66498.1 AFU66498	Artibeus fimbriatus cytochrome b (cytb...	50	2e-05
gb U63061.1 BBU63061	Brachyramphus brevirostris cytochrome ...	50	2e-05
gb U63060.1 BBU63060	Brachyramphus brevirostris cytochrome ...	50	2e-05
gb U63059.1 BBU63059	Brachyramphus brevirostris cytochrome ...	50	2e-05
gb U63058.1 BBU63058	Brachyramphus brevirostris cytochrome ...	50	2e-05
gb U58386.1 SJU58386	Scolomys juruaense cytochrome b (cyt-b...	50	2e-05
gb L11905.1 CGYMTCTB9D	Cratogeomys gymnuris mitochondrial c...	50	2e-05
gb U34672.1 MNU34672	Metachirus nudicaudatus cytochrome b l...	50	2e-05
gb U34671.1 MNU34671	Metachirus nudicaudatus cytochrome b l...	50	2e-05
emb Y14951.1 MTY14951	Capreolus capreolus mitochondrial cyt...	50	2e-05
emb Y14371.1 MTCCCYTB	Capreolus capreolus mitochondrial cyt...	50	2e-05
gb L11909.1 CGYMTCTB9H	Cratogeomys tylosinus mitochondrial...	50	2e-05
gb L11901.1 PPGMTCTB9B	Geomys bursarius juggosicularis mito...	50	2e-05
gb L11904.1 CGYMTCTB9C	Cratogeomys goldmani goldmani mitoch...	50	2e-05
emb X94928.1 SPCYTB	S. putorius mitochondrial DNA for cytoch...	50	2e-05
gb U46770.1 ARU46770	Anthus richardi cytochrome b gene, mit...	50	2e-05
gb U46769.1 ABU46769	Anthus berthelotii cytochrome b gene, ...	50	2e-05
gb U46183.1 SSU46183	Sciurus stramineus cytochrome b gene, ...	50	2e-05
emb Y10728.1 PSMY10728	P. schwarzi mitochondrial cytb gene, ...	50	2e-05
emb X95768.1 NLMCB	N. leucopterus mitochondrial cytochrome b...	50	2e-05
emb X95767.1 NGRIMCB	N. griseus mitochondrial cytochrome b gene	50	2e-05
emb X86763.1 MTVGCT26	V. gryphus mitochondrial cytb gene	50	2e-05
emb X86754.1 MTLCCYT17	L. crumeniferus mitochondrial cytb gene	50	2e-05
emb X86743.1 MTQACT6	C. aura mitochondrial cytb gene	50	2e-05
dbj AB035242.1 AB035242	Pantodon buchholzi mitochondrial cy...	50	2e-05
emb X50946.1 MITDCB33	T. dorbignyi mitochondrial gene for c...	50	2e-05
emb AJ000029.1 MIRTCYB29	Rangifer tarandus mitochondrial cy...	50	2e-05
emb X82302.1 MIFFCYTB9	P. fasciata mitochondrial cytochrome ...	50	2e-05
emb X56291.1 MIOHCYTB	O. hemionus mitochondrial cytb gene fo...	50	2e-05
emb X56284.1 MIOACYTB	O. aries mitochondrial cytb gene for c...	50	2e-05
emb AJ000022.1 MIMSCYB22	Dama dama mitochondrial cytb gene	50	2e-05
emb X72005.1 MILWCYTB	L. weddelli mitochondrial gene for cyt...	50	2e-05
emb Y08814.1 MIHLCTB9	H. liberiensis mitochondrial cytochr...	50	2e-05
emb X60942.1 MIGTCB33	Gymnorhina tibicen mitochondrial gene...	50	2e-05
emb X56290.1 MIDDCYTB	D. dama mitochondrial cytb gene for cy...	50	2e-05
emb AJ000021.1 MICECYB21	Cervus elaphus mitochondrial cytb ...	50	2e-05
emb AJ000024.1 MICCCYB24	Capreolus capreolus mitochondrial ...	50	2e-05
emb V00654.1 MIETXK	Bos taurus complete mitochondrial genome	50	2e-05
emb X36286.1 MIAACYTB3A	A. americana mitochondrial cytb gene ...	50	2e-05
gb L19718.1 AIUMTCYTB	Artibeus lituratus mitochondrial cyto...	50	2e-05
gb U27543.1 BRU27543	Balearica regulorum cytochrome b (cytb...	50	2e-05
dbj AB030025.1 AB030025	Sciurus stramineus mitochondrial cy...	50	2e-05
gb U18258.1 SCU18258	Spharagemon campestris cytochrome b ge...	50	2e-05
gb U18257.1 SCU18257	Spharagemon coliare cytochrome b gene...	50	2e-05
gb U18253.1 TPU18253	Trimerotropis pistrinaria cytochrome b...	50	2e-05
gb U18250.1 CPU18250	Camnula pellucida cytochrome b gene, m...	50	2e-05
gb U17904.1 CCU17904	Circotectix carlinianus mitochondrial ...	50	2e-05
dbj D84202.1 GOTMTCB8	Capra falconeri mitochondrial DNA for...	50	2e-05
dbj D82889.1 D82889	Bos javanicus mitochondrial DNA for cyt...	50	2e-05
dbj D32195.1 CCRMTCB25	Capricornis sumatrensis mitochondrial...	50	2e-05
dbj D32191.1 CCRMTCB21	Capricornis crispus mitochondrial ge...	50	2e-05
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dbj AB021095.1 AB021095	Cervus nippon yezoensis mitochondri...	50	2e-05
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dbj AB021092.1 AB021092	Cervus nippon mageshimae mitochondr...	50	2e-05
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dbj AB001612.1 AB001612	Cervus elaphus mitochondrial DNA fo...	50	2e-05
dbj D84205.1 SHPMTCB8E	Sheep mitochondrial DNA for cytochrom...	50	2e-05
dbj D84201.1 SHPMTCB8C	Ovis musimon mitochondrial DNA for cy...	50	2e-05
dbj D34625.1 BOVMTCB8	Bos javanicus mitochondrial gene for ...	50	2e-05
dbj D34623.1 BOVMTCB8A	Bovine mitochondrial gene for cytochr...	50	2e-05
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dbj D31125.1 NACMTCB26	Nemorhaedus goral mitochondrial gene...	50	2e-05

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dbj AB021096.1 AB021096	Cervus elaphus canadensis mitochond...	50	2e-05
dbj AB021093.1 AB021093	Cervus nippon nippon mitochondrial ...	50	2e-05
dbj AB021090.1 AB021090	Cervus nippon pulchellus mitochondr...	50	2e-05
dbj AB006539.1 AB006539	Dinocyon semicarinatus mitochondrial...	50	2e-05
dbj AB006800.1 AB006800	Ovis aries mitochondrial DNA for cy...	50	2e-05
gb L12762.1 LDHMTCTB	Lepidochelys kempi (LE-3) mitochondri...	50	2e-05
gb L08032.1 CPLMTCYB	Carcharias plumbeus mitochondrial ...	50	2e-05
gb L28941.1 URRCYS	Uroderma bilobatum cytochrome b gene, 5'...	50	2e-05
gb L28937.1 CDECYB	Chiroderma doriae cytochrome b gene, 5' end	50	2e-05
emb AJ010056.1 CPY010056	Capra pyrenaica (individual 12) mi...	50	2e-05
emb AJ010054.1 CPY010054	Capra pyrenaica (individual 11) mi...	50	2e-05
emb AJ010053.1 CPY010053	Capra pyrenaica (individual 10) mi...	50	2e-05
emb AJ010052.1 CPY010052	Capra pyrenaica (individual 9) mit...	50	2e-05
emb AJ010051.1 CPY010051	Capra pyrenaica (individual 8) mit...	50	2e-05
emb AJ010050.1 CPY010050	Capra pyrenaica (individual 7) mit...	50	2e-05
emb AJ010049.1 CPY010049	Capra pyrenaica (individual 6) mit...	50	2e-05
emb AJ010048.1 CPY010048	Capra pyrenaica (individual 5) mit...	50	2e-05
emb AJ010047.1 CPY010047	Capra pyrenaica (individual 4) mit...	50	2e-05
emb X95777.1 CLMCE	C. longirostris mitochondrial cytochrome ...	50	2e-05
emb AJ009879.1 CIB9879	Capra ibex nubiana mitochondrial cyt...	50	2e-05
emb AJ010055.1 CIB010055	Capra ibex (individual 1) ibex mit...	50	2e-05
gb U08946.1 CAU08946	Coragyps atratus mitochondrion cytochr...	50	2e-05
gb U08945.1 CEU08945	Cathartes burrovianus mitochondrion cy...	50	2e-05
gb U08944.1 VGU08944	Vultur gryphus mitochondrion cytochrom...	50	2e-05
gb U08941.1 PAU08941	Platalea alba mitochondrion cytochrome...	50	2e-05
gb U08940.1 PRU08940	Phoenicopterus ruber mitochondrion cyt...	50	2e-05
emb X95775.1 ACMCE	A. cristatus mitochondrial cytochrome b gene	50	2e-05
emb X95774.1 ABMCE	A. bennettii mitochondrial cytochrome b gene	50	2e-05
emb X95764.1 AAMCE	A. albertisi mitochondrial cytochrome b gene	50	2e-05
gb AF040383.1 AF040383	Alces alces cytochrome b (cytb) gene...	45	8e-05
gb AF232023.1 AF232023	Tamandua tetradactyla clone 7 cytoch...	45	3e-04
gb AF232022.1 AF232022	Tamandua tetradactyla clone 6 mitoch...	45	3e-04
gb AF232021.1 AF232021	Tamandua tetradactyla clone 5 cytoch...	45	3e-04
gb AF157456.1 AF157456	Lepus timidus cytochrome b (Cyb) gen...	45	3e-04
gb AF157455.1 AF157455	Lepus granatensis cytochrome b (Cyb)...	45	3e-04
gb AF157454.1 AF157454	Lepus corsicanus haplotype 1 cytochr...	45	3e-04
gb AF157453.1 AF157453	Lepus corsicanus haplotype 3 cytochr...	45	3e-04
gb AF157450.1 AF157450	Lepus europaeus cytochrome b (Cyb) g...	45	3e-04
gb AF231664.1 AF231664	Tylosurus crocodilus crocodilus cyto...	45	3e-04
gb AF231663.1 AF231663	Tylosurus crocodilus clone STR1-1637...	45	3e-04
gb AF231662.1 AF231662	Tylosurus crocodilus clone KB-156 cy...	45	3e-04
gb AF231660.1 AF231660	Tylosurus acus pacificus cytochrome ...	45	3e-04
gb AF231659.1 AF231659	Tylosurus acus melanotus clone STR1-...	45	3e-04
gb AF231658.1 AF231658	Tylosurus acus melanotus clone STR1-...	45	3e-04
gb AF231657.1 AF231657	Tylosurus acus imperialis cytochrome...	45	3e-04
gb AF231656.1 AF231656	Tylosurus acus acus cytochrome b oxi...	45	3e-04
gb AF231644.1 AF231644	Strongylura hubbsi cytochrome b oxid...	45	3e-04
gb AF231639.1 AF231639	Ablennes hians cytochrome b oxidase ...	45	3e-04
gb AF232019.1 AF232019	Tamandua tetradactyla clone 3 cytoch...	45	3e-04
gb AF232017.1 AF232017	Tamandua tetradactyla clone 1 cytoch...	45	3e-04
gb AF232014.1 AF232014	Myiodon darwini cytochrome b gene, ...	45	3e-04
gb AF318564.1 AF318564	Alligator mississippiensis isolate S...	45	3e-04
gb AF318563.1 AF318563	Alligator mississippiensis isolate S...	45	3e-04
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gb AF318561.1 AF318561	Alligator mississippiensis isolate C...	45	3e-04
gb AF318560.1 AF318560	Alligator mississippiensis isolate C...	45	3e-04
gb AF318559.1 AF318559	Alligator mississippiensis isolate A...	45	3e-04
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gb AF318550.1 AF318550	Alligator mississippiensis isolate F...	45	3e-04
gb AF318549.1 AF318549	Alligator mississippiensis isolate F...	45	3e-04
gb AF318548.1 AF318548	Alligator mississippiensis isolate F...	45	3e-04
gb AF318041.1 AF318041	Sorex monticolus specimen-voucher AF...	45	3e-04



gb AF126272.1 AF126272	Myospalax myospalax cytochrome b (cy...	46	3e-04
gb AF126271.1 AF126271	Myospalax psilurus isolate 2 cytochr...	46	3e-04
gb AF126270.1 AF126270	Myospalax psilurus isolate 1 cytochr...	46	3e-04
gb AF126266.1 AF126266	Eospalax fontanieri isolate 4 cytoc...	46	3e-04
emb AJ004340.1 ADAJ4340	Acrocephalus dumetorum mitochondria...	44	0.001
emb AJ004264.1 ADAJ4264	Acrocephalus dumetorum mitochondria...	44	0.001

## Alignments

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<u>J011394</u>	14911	.....	14935
<u>AF193830</u>	302	.....	326
<u>U89181</u>	401	.....	425
<u>U89171</u>	401	.....	425
<u>AF217833</u>	371	.....	395
<u>AF217822</u>	374	.....	398
<u>AF217813</u>	374	.....	398
<u>AF220408</u>	413	.....	437
<u>AF126430</u>	398	.....	422
<u>AF090337</u>	15123	.....	15147
<u>AF059111</u>	305	.....	329
<u>AF059053</u>	305	.....	329
<u>AF099308</u>	303	.....	327
<u>AF099295</u>	303	.....	327
<u>AF099294</u>	303	.....	327
<u>AF099293</u>	303	.....	327
<u>AF160610</u>	398	.....	422
<u>AF036280</u>	398	.....	422
<u>AF036277</u>	398	.....	422
<u>AF036274</u>	398	.....	422
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<u>AF194216</u>	302	.....	326
<u>NC_002009</u>	14547	.....	14571
<u>NC_001941</u>	14556	.....	14580
<u>NC_000877</u>	15123	.....	15147
<u>NC_000846</u>	14038	.....	14062
<u>U27551</u>	401	.....	425
<u>AF089058</u>	281	.....	305
<u>AF089055</u>	281	.....	305
<u>AF089054</u>	281	.....	305
<u>AF089046</u>	281	.....	305
<u>AF089042</u>	272	.....	296
<u>AF089039</u>	281	.....	305
<u>AF089037</u>	281	.....	305
<u>AF089026</u>	281	.....	305
<u>AF089025</u>	281	.....	305
<u>AF089024</u>	281	.....	305
<u>AF089023</u>	281	.....	305
<u>AF089021</u>	281	.....	305
<u>AF089020</u>	281	.....	305
<u>AF089016</u>	281	.....	305
<u>AF089013</u>	281	.....	305
<u>AF089012</u>	281	.....	305
<u>AF089008</u>	281	.....	305
<u>AF089006</u>	257	.....	281
<u>AF089005</u>	281	.....	305
<u>AF108696</u>	398	.....	422
<u>AF108685</u>	392	.....	416
<u>AF108677</u>	398	.....	422
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<u>AF145511</u>	169	.....	193
<u>U89627</u>	360	.....	384
<u>U89623</u>	360	.....	384
<u>AF181470</u>	303	.....	327
<u>AF084075</u>	398	.....	422
<u>U90303</u>	398	.....	422
<u>U90302</u>	398	.....	422
<u>U90301</u>	398	.....	422
<u>U90300</u>	398	.....	422
<u>AF018883</u>	392	.....	416
<u>AF019268</u>	392	.....	416
<u>AF019267</u>	392	.....	416
<u>S49215</u>	56	.....	80
<u>AF138698</u>	398	.....	422
<u>AF138693</u>	398	.....	422
<u>AF068121</u>	401	.....	425

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<u>AF022063</u>	398	.....	422
<u>AF022062</u>	398	.....	422
<u>AF022060</u>	398	.....	422
<u>AF022057</u>	398	.....	422
<u>AF113500</u>	384	.....	408
<u>AF113499</u>	363	.....	387
<u>U69845</u>	374	.....	398
<u>U69810</u>	374	.....	398
<u>U69808</u>	374	.....	398
<u>U69799</u>	374	.....	398
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<u>U69795</u>	374	.....	398
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<u>U69793</u>	374	.....	398
<u>U69792</u>	374	.....	398
<u>U69790</u>	374	.....	398
<u>U69786</u>	374	.....	398
<u>U69784</u>	374	.....	398
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<u>U69746</u>	374	.....	398
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<u>AF139057</u>	398	.....	422
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<u>AF061340</u>	14547	.....	14571
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<u>AF076048</u>	401	.....	425
<u>AF076047</u>	401	.....	425
<u>U83314</u>	401	.....	425
<u>U83318</u>	401	.....	425
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<u>U37302</u>	303	.....	327
<u>U37296</u>	303	.....	327
<u>U37289</u>	303	.....	327
<u>U37286</u>	303	.....	327
<u>U37104</u>	303	.....	327
<u>U37087</u>	303	.....	327
<u>U87525</u>	380	.....	404
<u>U87524</u>	385	.....	409
<u>U87523</u>	354	.....	378
<u>U87522</u>	379	.....	403
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<u>V17863</u>	329	.....	353
<u>V17862</u>	398	.....	422
<u>V17860</u>	398	.....	422
<u>V17859</u>	329	.....	353
<u>U65274</u>	398	.....	422
<u>U65267</u>	398	.....	422
<u>U65260</u>	398	.....	422
<u>U65191</u>	398	.....	422

<u>AF034739</u>	398	.....	422
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<u>AF034735</u>	398	.....	422
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<u>AF057132</u>	396	.....	422
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<u>AJ293412</u>	398	.....	422
<u>AJ293418</u>	398	.....	422
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<u>Y15697</u>	432	.....	456
<u>Y15696</u>	432	.....	456
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<u>AF015758</u>	303	.....	327
<u>AF015756</u>	303	.....	327
<u>AF015754</u>	303	.....	327
<u>U76052</u>	401	.....	425
<u>AJ236814</u>	398	.....	422
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<u>U83156</u>	302	.....	326
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<u>AJ277676</u>	299	.....	323
<u>AJ277675</u>	299	.....	323
<u>AJ277672</u>	299	.....	323
<u>AJ277671</u>	299	.....	323
<u>Y11832</u>	14568	.....	14592
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<u>AJ388468</u>	305	.....	329
<u>AJ388459</u>	305	.....	329
<u>U46167</u>	398	.....	422
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<u>AJ245675</u>	400	.....	424
<u>AJ245674</u>	400	.....	424
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<u>U66502</u>	398	.....	422
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<u>U66500</u>	398	.....	422
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<u>Y14371</u>	398	.....	422
<u>L11909</u>	398	.....	422
<u>L11901</u>	398	.....	422
<u>L11904</u>	398	.....	422
<u>X94928</u>	398	.....	422
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<u>X86763</u>	299	.....	323
<u>X86754</u>	299	.....	323
<u>X86743</u>	299	.....	323
<u>AB035242</u>	398	.....	422
<u>X60946</u>	302	.....	326
<u>AJ000029</u>	398	.....	422
<u>X82302</u>	398	.....	422
<u>X56291</u>	398	.....	422
<u>X56284</u>	398	.....	422
<u>AJ000022</u>	398	.....	422
<u>X72005</u>	398	.....	422
<u>Y08814</u>	398	.....	422
<u>X60942</u>	302	.....	326
<u>X56290</u>	398	.....	422
<u>AJ000021</u>	398	.....	422
<u>AJ000024</u>	398	.....	422
<u>V00654</u>	14911	.....	14915
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<u>L19718</u>	398	.....	422
<u>U27543</u>	401	.....	425
<u>AB030025</u>	343	.....	367
<u>U18258</u>	169	.....	193
<u>U18257</u>	169	.....	193
<u>U18253</u>	169	.....	193
<u>U18250</u>	169	.....	193
<u>U17904</u>	169	.....	193
<u>DB4202</u>	398	.....	422
<u>DB2889</u>	398	.....	422
<u>Q12195</u>	243	.....	267
<u>Q12191</u>	398	.....	422
<u>AB021098</u>	198	.....	422
<u>AB021097</u>	198	.....	422
<u>AB021095</u>	198	.....	422
<u>AB021094</u>	198	.....	422
<u>AB021093</u>	198	.....	422
<u>AB021091</u>	198	.....	422

<u>AB001612</u>	398	.....	422
<u>D84205</u>	398	.....	422
<u>D84203</u>	398	.....	422
<u>D34636</u>	398	.....	422
<u>D34635</u>	398	.....	422
<u>D32198</u>	243	.....	267
<u>D32196</u>	243	.....	267
<u>D32192</u>	398	.....	422
<u>AB021099</u>	398	.....	422
<u>AB021096</u>	398	.....	422
<u>AB021093</u>	398	.....	422
<u>AB021090</u>	398	.....	422
<u>AB008539</u>	15302	.....	15326
<u>AB006800</u>	398	.....	422
<u>L12763</u>	260	.....	284
<u>L08032</u>	401	.....	425
<u>L28941</u>	398	.....	422
<u>L28917</u>	398	.....	422
<u>AJ010056</u>	269	.....	293
<u>AJ010054</u>	269	.....	293
<u>AJ010053</u>	269	.....	293
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<u>AJ010051</u>	269	.....	293
<u>AJ010050</u>	269	.....	293
<u>AJ010049</u>	269	.....	293
<u>AJ010048</u>	269	.....	293
<u>AJ010047</u>	269	.....	293
<u>X95777</u>	407	.....	431
<u>AJ009879</u>	269	.....	293
<u>AJ010055</u>	269	.....	293
<u>U08946</u>	303	.....	327
<u>U08945</u>	303	.....	327
<u>U08944</u>	303	.....	327
<u>U08941</u>	303	.....	327
<u>U08940</u>	303	.....	327
<u>X95775</u>	303	.....	327
<u>X95774</u>	303	.....	327
<u>X95764</u>	303	.....	327
<u>AF040383</u>	287	.....	310
<u>AF232023</u>	400	.....	422
<u>AF232022</u>	400	.....	422
<u>AF232021</u>	400	.....	422
<u>AF157466</u>	322	.....	344
<u>AF157465</u>	324	.....	346
<u>AF157464</u>	324	.....	346
<u>AF157463</u>	324	.....	346
<u>AF157460</u>	321	.....	343
<u>AF231664</u>	400	.....	422
<u>AF231663</u>	400	.....	422
<u>AF231662</u>	400	.....	422
<u>AF231660</u>	400	.....	422
<u>AF231659</u>	400	.....	422
<u>AF231658</u>	400	.....	422
<u>AF231657</u>	400	.....	422
<u>AF231656</u>	400	.....	422
<u>AF231644</u>	400	.....	422
<u>AF231639</u>	400	.....	422
<u>AF232019</u>	400	.....	422
<u>AF232017</u>	400	.....	422
<u>AF232014</u>	400	.....	422
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<u>AF118562</u>	344	.....	366
<u>AF118561</u>	344	.....	366
<u>AF118560</u>	344	.....	366
<u>AF118559</u>	344	.....	366
<u>AF118558</u>	344	.....	366
<u>AF118557</u>	381	.....	403
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<u>AF118554</u>	381	.....	403

<u>AF118551</u>	381	.....	403
<u>AF118552</u>	381	.....	403
<u>AF118551</u>	381	.....	403
<u>AF118550</u>	381	.....	403
<u>AF118549</u>	381	.....	403
<u>AF118548</u>	381	.....	403
<u>AF238041</u>	400	.....	422
<u>AF326272</u>	400	.....	422
<u>AF326271</u>	400	.....	422
<u>AF326270</u>	400	.....	422
<u>AF326266</u>	400	.....	422
<u>AJ004340</u>	302	.....n.....	326
<u>AJ004264</u>	302	.....n.....	326

Database: nt

Posted date: Mar 2, 2001 12:20 AM

Number of letters in database: 2,863,827,885

Number of sequences in database: 807,597

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 39355

Number of Sequences: 807597

Number of extensions: 39355

Number of successful extensions: 15066

Number of sequences better than 10.0: 5706

length of query: 25

length of database: 2,863,827,885

effective HSP length: 17

effective length of query: 8

effective length of database: 2,850,098,736

effective search space: 22800789888

effective search space used: 22800789888

T: 0

A: 30

X1: 6 (11.9 bits)

X2: 15 (29.7 bits)

S1: 12 (24.3 bits)

S2: 16 (32.2 bits)

**Table 11. BLAST analysis of primers 'mcb869' in *nr* database of NCBI. It demonstrates that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer.**



BLASTN 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593033-24247-14777

Query-

(26 letters)

Database: nt

807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reports

Distribution of 500 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments





## Sequences producing significant alignments:

Score S  
(bits) Value

qb AF189111.1 AF189111	Cryptotermes austrinus cytochrome b ...	52	6e-06
qb U86834.1 U86834	Phyllosticta wolffsohni MSB 67270 cytochrome...	52	6e-06
qb AF123633.1 AF123633	Perissoccephalus tricolor cytochrome ...	52	6e-06
qb AF123617.1 AF123617	Pipreola arcuata cytochrome b gene, ...	52	6e-06
qb AF127202.1 AF127202	Hylopetes fulviventris cytochrome b ...	52	6e-06
qb AF127194.1 AF127194	Grallaria guatemalensis cytochrome b...	52	6e-06
qb AF217828.1 AF217828	Aspidelaps scutatus cytochrome b gen...	52	6e-06
qb AF160578.1 AF160578	Hypogeomys antimenae Hant555 cytochro...	52	6e-06
qb AF009931.2 AF009931	Archocentrus centrarchus cytochrome ...	52	6e-06
qb AF091629.1 AF091629	Antilocapra americana cytochrome b (...	52	6e-06
qb AF034967.1	Sigmoceros lichtensteinii cytochrome b gene,...	52	6e-06
qb AF038290.1 AF038290	Antechinus sp. cytochrome b gene, mi...	52	6e-06
qb U07577.1 AMU07577	Antechinus melanurus mitochondrion cyt...	52	6e-06
qb U81343.1 CFU81343	Chelus fimbriata cytochrome b gene, mi...	52	6e-06
emb AJ222681.1 ABCYT08	Alcelaphus buselaphus mitochondrial ...	52	6e-06
qb M99464.1 PNZMTCYT8	Planigale sp. cytochrome b gene, comp...	52	6e-06
emb AJ225116.1 DNJ225116	Dryomys nitedula mitochondrial gen...	52	6e-06
qb U25738.1 PRU25738	Paradisaea raggiana cytochrome b gene,...	52	6e-06
qb U25736.1 PRU25736	Paradisaea rubra cytochrome b gene, mi...	52	6e-06
qb U15202.1 SMU15202	Seleucidis melanoleuca mitochondrion c...	52	6e-06
qb U15204.1 PR15204	Paradisaea raggiana mitochondrion cytoc...	52	6e-06
emb X56290.1 MIDDCYT8	D.dama mitochondrion cytb gene for cy...	52	6e-06
emb X56286.1 MIAACYT8A	A.americana mitochondrion cytb gene ...	52	6e-06
dbj D88639.1 D88639	Anoa depressicornis mitochondrial DNA f...	52	6e-06
dbj D82890.1 D82890	Bubalus depressicornis mitochondrial DN...	52	6e-06
qb AF119261.1 AF119261	Peromyscus maniculatus cytochrome b ...	46	3e-04
qb AF123615.1 AF123615	Rupicola rupicola cytochrome b gene,...	46	3e-04
qb AF160603.1 AF160603	Apodemus sylvaticus Asy1588 cytochro...	46	3e-04
qb U62697.1 CCOLCYT82	Charadrius collaris cytochrome b (cyt...	46	3e-04
qb U62685.1 CSICCYT82	Charadrius biniactus cytochrome b (cy...	46	3e-04
qb AF022071.1	Madoqua guentheri cytochrome b (cytb) gene, ...	46	3e-04
qb AF022070.1	Madoqua kirkii cytochrome b (cytb) gene, mit...	46	3e-04
qb U83317.1 PSU83317	Polihierax semitorquatus cytochrome b ...	46	3e-04
qb U37293.1 CCU37293	Cephus columba cytochrome b gene, mit...	46	3e-04
qb U37292.1 CCU37292	Cephus carbo cytochrome b gene, mitoc...	46	3e-04
qb U37291.1 SMU37291	Brachyramphus marmoratus perdix cytoch...	46	3e-04
qb AF082055.1 AF082055	Rupicola rupicola cytochrome b gene,...	46	3e-04
qb U72770.1 JMU72770	Jabiru mycteria cytochrome b gene, mit...	46	3e-04
qb U07578.1 DCU07578	Dasyercus cristicauda mitochondrion c...	46	3e-04
qb AF031908.1 GOCCTCYT83	Geopsittacus occidentalis cytochrom...	46	3e-04
emb AJ004231.1 SBAJ4231	Sula bassana mitochondrial cytb gen...	46	3e-04
emb AJ004230.1 SBAJ4230	Sula bassana mitochondrial cytb gen...	46	3e-04
emb AJ004229.1 SBAJ4229	Sula bassana mitochondrial cytb gen...	46	3e-04
emb AJ004232.1 SBAJ4232	Sula bassana mitochondrial cytb gen...	46	3e-04
qb U88865.1	Pomacentrus sp. cytochrome b (cytb) gene, mito...	46	3e-04
qb U90001.1 MSU90001	Morus bassanus cytochrome b gene, mito...	46	3e-04
qb U63057.1 SMU63057	Brachyramphus marmoratus perdix cytoch...	46	3e-04
dbj AB036404.1 AB036404	Rana porosa brevipoda mitochondrial...	46	3e-04
dbj AB036402.1 AB036402	Rana porosa brevipoda mitochondrial...	46	3e-04
dbj AB036400.1 AB036400	Rana porosa brevipoda mitochondrial...	46	3e-04
dbj AB036398.1 AB036398	Rana porosa porosa mitochondrial DN...	46	3e-04
qb U19611.1 JMU19611	Jabiru mycteria cytochrome b gene, mit...	46	3e-04
emb X22519.1 HACT8	H.ampullatus cytochrome b gene (comple...	46	3e-04
qb U08014.1 GAEMTCYT8A	Galeocerdo cuvier mitochondrial cyto...	46	3e-04
qb U08013.1 CPLMTCYT88	Carcharias porosus mitochondrial c...	46	3e-04
qb AY015012.1	Crypturellus tataupa mitochondrion, partial ...	44	0.001
qb AF074591.1 AF074591	Petrochelidon pyrrhonota cytochrome ...	44	0.001
qb AY005212.1	Pooeciza whitii isolate 2 cytochrome b (cytb)...	44	0.001
qb AY005211.1	Pooeciza whitii isolate 1 cytochrome b (cytb)...	44	0.001
qb AF1892132.1 AF1892132	Cryptotermes tropicalis cytochrome b...	44	0.001
qb AF1892130.1 AF1892130	Cryptotermes secundus cytochrome b (...	44	0.001
qb AF1892119.1 AF1892119	Cryptotermes primus isolate 2 cytoch...	44	0.001
qb AF1892117.1 AF1892117	Cryptotermes primus isolate 1 cytoch...	44	0.001
qb AF1892115.1 AF1892115	Cryptotermes dudleyi cytochrome b (Cy...	44	0.001
qb AF1892113.1 AF1892113	Ovis canadensis cytochrome b gene, p...	44	0.001
qb AF1892112.1 AF1892112	Ovis canadensis canadensis cytochrom...	44	0.001
qb AF1892111.1 AF1892111	Ovis canadensis nelsoni cytochrome b ...	44	0.001
qb AF291272.1 AF291272	Vireo cacaecia cacaecia apoclinus...	44	0.001

gb AF081989.1 AF081989	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081988.1 AF081988	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081987.1 AF081987	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081986.1 AF081986	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081985.1 AF081985	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081984.1 AF081984	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081983.1 AF081983	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081982.1 AF081982	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081981.1 AF081981	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081980.1 AF081980	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081979.1 AF081979	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081978.1 AF081978	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081977.1 AF081977	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081976.1 AF081976	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081975.1 AF081975	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081974.1 AF081974	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081973.1 AF081973	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081972.1 AF081972	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081971.1 AF081971	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081970.1 AF081970	Vireo solitarius alticola country US...	44	0.001
gb AF081969.1 AF081969	Vireo solitarius alticola country US...	44	0.001
gb AF081968.1 AF081968	Vireo solitarius alticola country US...	44	0.001
gb AF081967.1 AF081967	Vireo solitarius alticola country US...	44	0.001
gb AF081966.1 AF081966	Vireo solitarius solitarius specimen...	44	0.001
gb AF081965.1 AF081965	Vireo solitarius solitarius specimen...	44	0.001
gb AF081964.1 AF081964	Vireo solitarius solitarius specimen...	44	0.001
gb AF081962.1 AF081962	Vireo flavifrons specimen-voucher LS...	44	0.001
gb AF081961.1 AF081961	Vireo flavifrons specimen-voucher LS...	44	0.001
gb AF081960.1 AF081960	Vireo leucophrys leucophrys specimen...	44	0.001
gb AF081959.1 AF081959	Vireolanius leucotis leucotis cytoch...	44	0.001
gb AF112405.2 AF112405	Barbus anoplus cytochrome b (cytb) g...	44	0.001
gb AF144317.1 AF144317	Amphiprion ocellaris isolate 3 haplo...	44	0.001
gb AF144316.1 AF144316	Amphiprion ocellaris haplotype 3DH11...	44	0.001
gb AF144315.1 AF144315	Amphiprion ocellaris haplotype 3DH15...	44	0.001
gb AF144314.1 AF144314	Amphiprion ocellaris isolate 2 haplo...	44	0.001
gb AF144313.1 AF144313	Amphiprion ocellaris isolate 1 haplo...	44	0.001
gb AF144312.1 AF144312	Amphiprion ocellaris haplotype 3DH12...	44	0.001
gb AF144311.1 AF144311	Amphiprion ocellaris haplotype 3DH1...	44	0.001
gb AF144310.1 AF144310	Amphiprion ocellaris isolate 2 haplo...	44	0.001
gb AF144309.1 AF144309	Amphiprion ocellaris isolate 1 haplo...	44	0.001
ref NC 001567.1	Bos taurus mitochondrion, complete genome	44	0.001
gb AF212124.1 AF212124	Anolis schwartzi cytochrome b gene, ...	44	0.001
gb AF182706.1 AF182706	Phapitreron amethystina cytochrome b...	44	0.001
gb AF010406.1 AF010406	Ovis aries complete mitochondrial ge...	44	0.001
gb AF096452.1 AF096452	Platysteira cyanea cytochrome b gene...	44	0.001
gb AF281619.1 AF281619	Elaphe obsoleta LSUMZ19162 cytochrom...	44	0.001
gb AF281618.1 AF281618	Elaphe obsoleta LSUMZ H15896 cytochr...	44	0.001
gb AF281608.1 AF281608	Elaphe obsoleta LSUMZ H14782 cytochr...	44	0.001
gb AF281602.1 AF281602	Elaphe obsoleta LSUMZ H1388 cytochro...	44	0.001
gb AF110069.1 AF110069	Elaenia martinica cytochrome b gene...	44	0.001
gb AF146616.1 AF146616	Actophilornis africanus cytochrome b...	44	0.001
gb AF271410.1 AF271410	Galago moholi cytochrome b (cyt b) g...	44	0.001
gb AF290139.1 AF290139	Peucedramus taeniatus cytochrome b (...)	44	0.001
ref NC 002504.1	Lama pacos mitochondrion, complete genome	44	0.001
gb AF163901.1 AF163901	Microtus ochrogaster cytochrome b ge...	44	0.001
gb AF119253.1 AF119253	Myopus schisticolor cytochrome b gen...	44	0.001
gb AF119259.1 AF119259	Synaptomys borealis cytochrome b gen...	44	0.001
gb AF288454.1 AF288454	Nyctereutes procyonoides korensis c...	44	0.001
gb AF163895.1 AF163895	Microtus gregalis cytochrome B (cytB...	44	0.001
gb AF123647.1 AF123647	Machaeropterus regulus ecriolatus cy...	44	0.001
gb AF123646.1 AF123646	Machaeropterus pyrocephalus cytochro...	44	0.001
gb AF123645.1 AF123645	Xenopipo acronitens cytochrome b gen...	44	0.001
gb AF123644.1 AF123644	Pipra fasciata cytochrome b gene...	44	0.001
gb AF123643.1 AF123643	Pyroderus ecutatus cytochrome b gene...	44	0.001
gb AF123642.1 AF123642	Cephalopterus ornatus cytochrome b g...	44	0.001
gb AF123641.1 AF123641	Turdampella cryptolophus cytochrome ...	44	0.001
gb AF123640.1 AF123640	Porphyrolaema porphyrolaema cytochro...	44	0.001
gb AF123639.1 AF123639	Ampelioides techudii cytochrome b ge...	44	0.001
gb AF123638.1 AF123638	Elphidotia chlorolepis cytochrome b...	44	0.001
gb AF123637.1 AF123637	Rupicola peruviana cytochrome b gene...	44	0.001
gb AF123636.1 AF123636	Oellonnia eclestici cytochrome b gene...	44	0.001

gb AF127201.1 AF127201	Myrmothera campanisona cytochrome b ...	44	0.001
gb AF127192.1 AF127192	Grallaria ruficapilla cytochrome b g...	44	0.001
gb AF127189.1 AF127189	Grallaria varia cytochrome b gene, p...	44	0.001
gb AF197849.1 AF197849	Sericornis frontalis cytochrome b ge...	44	0.001
gb AF197847.1 AF197847	Pardalotus striatus cytochrome b gen...	44	0.001
ref NC 000889.1	Hippopotamus amphibius mitochondrion, comp...	44	0.001
ref NC 002079.1	Carassius auratus mitochondrion, complete ...	44	0.001
ref NC 001794.1	Macropus robustus mitochondrion, complete ...	44	0.001
ref NC 001610.1	Didelphis virginiana mitochondrion, comple...	44	0.001
gb AF201612.1 AF201612	Stomatorhinus sp. CU79703 cytochrome...	44	0.001
gb AF097931.1 AF097931	Amphiprion clarkii cytochrome b gene...	44	0.001
gb AF097927.1 AF097927	Amphiprion ocellaris cytochrome b ge...	44	0.001
gb J01394.1 BOVMT	Bos taurus mitochondrion, complete genome	44	0.001
gb AF168760.1 AF168760	Apalone spinifera isolate TXsc cytoc...	44	0.001
gb AF168759.1 AF168759	Apalone spinifera isolate TXki cytoc...	44	0.001
gb AF168758.1 AF168758	Apalone spinifera isolate TXcc cytoc...	44	0.001
gb AF168756.1 AF168756	Apalone spinifera isolate NMrg cytoc...	44	0.001
gb AF182381.1 AF182381	Petrochelidon rufocollaris isolate E...	44	0.001
gb AF182380.1 AF182380	Petrochelidon rufocollaris isolate E...	44	0.001
gb U89187.1 MMU89187	Momotus mexicanus cytochrome b (cytb) ...	44	0.001
gb AF193833.1 AF193833	Botaurus lentiginosus cytochrome b g...	44	0.001
gb AF193822.1 AF193822	Ardea alba cytochrome b gene, partia...	44	0.001
gb AF193821.1 AF193821	Ardea herodias cytochrome b gene, pa...	44	0.001
gb AF217837.1 AF217837	Paranaja multifasciata cytochrome b ...	44	0.001
gb AF217835.1 AF217835	Naja kaouthia cytochrome b gene, com...	44	0.001
gb AF217834.1 AF217834	Laticauda colubrina cytochrome b gen...	44	0.001
gb AF217831.1 AF217831	Calliophis japonicus cytochrome b ge...	44	0.001
gb AF217823.1 AF217823	Micruroides euryxanthus cytochrome b...	44	0.001
gb AF217819.1 AF217819	Drysdalia coronata cytochrome b gene...	44	0.001
gb AF217815.1 AF217815	Austrelaps superbus cytochrome b gen...	44	0.001
gb AF118156.1 AF118156	Teranura humeralis specimen-voucher ...	44	0.001
gb AF209938.1 AF209938	Euura atra isolate 62 cytochrome b g...	44	0.001
gb AF209933.1 AF209933	Euura atra isolate C cytochrome b ge...	44	0.001
gb AF059104.1 AF059104	Marmaronetta angustirostris cytochro...	44	0.001
gb AF059102.1 AF059102	Lophonetta specularoides cytochrome ...	44	0.001
gb AF059054.1 AF059054	Amazonetta brasiliensis cytochrome b...	44	0.001
gb AF192646.1 AF192646	Hippocampus barbouri haplotype PH.22...	44	0.001
gb AF192645.1 AF192645	Hippocampus barbouri haplotype PH.13...	44	0.001
gb AF160614.1 AF160614	Cricetomys gambianus Cgam518 cytochr...	44	0.001
gb AF160613.1 AF160613	Cricetomys emini Cemi511 cytochrome ...	44	0.001
gb AF160612.1 AF160612	Cricetomys emini Cemi530 cytochrome ...	44	0.001
gb AF160611.1 AF160611	Cricetomys emini Cemi537 cytochrome ...	44	0.001
gb AF160610.1 AF160610	Cricetomys emini Cemi536 cytochrome ...	44	0.001
gb AF160604.1 AF160604	Calomyscus bailwardi Cbal576 cytochr...	44	0.001
gb AF160560.1 AF160560	Eliurus majori Emaj642 cytochrome b ...	44	0.001
gb AF160559.1 AF160559	Eliurus majori Emaj641 cytochrome b ...	44	0.001
gb AF160558.1 AF160558	Eliurus majori Emaj639 cytochrome b ...	44	0.001
gb AF160557.1 AF160557	Eliurus majori Emaj638 cytochrome b ...	44	0.001
gb AF160555.1 AF160555	Eliurus majori Emaj614 cytochrome b ...	44	0.001
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gb AF160552.1 AF160552	Eliurus majori Emaj556 cytochrome b ...	44	0.001
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gb AF160550.1 AF160550	Eliurus majori Emaj443 cytochrome b ...	44	0.001
gb AF160549.1 AF160549	Eliurus majori Emaj444 cytochrome b ...	44	0.001
gb AF016287.1 AF016287	Damaliscus pygargus cytochrome b (cy...	44	0.001
gb AF016286.1 AF016286	Oryx leucorox cytochrome b (cytb) ge...	44	0.001
gb AF016283.1 AF016283	Antelope cervicapra cytochrome b (cy...	44	0.001
gb AF016281.1 AF016281	Antidorcas marsupialis cytochrome b ...	44	0.001
gb AF016278.1 AF016278	Tragelaphus oryx cytochrome b (cytb)...	44	0.001
gb AF016275.1 AF016275	Tragelaphus eucyceros cytochrome b (...)	44	0.001
gb AF016274.1	Tetracerus quadricornis cytochrome b (cytb) ...	44	0.001
ref NC 001941.1	Ovis aries mitochondrion, complete genome	44	0.001
gb AF109698.1 AF109698	Microcyzomys minutus cytochrome b (c...	44	0.001
gb AF109697.1 AF109697	Rhipidomys nitela cytochrome b (cytb)...	44	0.001
gb AF109677.1 AF109677	Thomomys daphne cytochrome b (cytb)...	44	0.001
gb AF109652.1 AF109652	Sceptrumys tumidus cytochrome b (cy...	44	0.001
gb AF042722.1 AF042722	Megamuntiacus vuquangensis cytochrom...	44	0.001
gb AF042719.1	Muntiacus muntjak cytochrome b gene, mitocho...	44	0.001
gb AF042718.1 AF042718	Stenella coeruleoalba cytochrome b g...	44	0.001
gb AF042717.1 AF042717	Stenella coeruleoalba cytochrome b g...	44	0.001

gb AF084074.1 AF084074	Lagenorhynchus albirostris cytochrom...	44	0.001
gb AF090750.1 AF090750	Gobio gobio balcanicus cytochrome b ...	44	0.001
gb AF157939.1 AF157939	Spermophilus columbianus columbianus...	44	0.001
gb AF157937.1 AF157937	Spermophilus washingtoni isolate S89...	44	0.001
gb AF157936.1 AF157936	Spermophilus washingtoni isolate S88...	44	0.001
gb AF157915.1 AF157915	Spermophilus richardsoni isolate S63...	44	0.001
gb AF157914.1 AF157914	Spermophilus richardsoni isolate S62...	44	0.001
gb AF157912.1 AF157912	Spermophilus undulatus isolate S60 c...	44	0.001
gb AF157906.1 AF157906	Spermophilus undulatus isolate S55 c...	44	0.001
gb AF157891.1 AF157891	Spermophilus elegans elegans isolate...	44	0.001
gb AF157882.1 AF157882	Spermophilus columbianus columbianus...	44	0.001
gb AF157859.1 AF157859	Spermophilus citellus isolate S118 c...	44	0.001
gb AF157858.1 AF157858	Spermophilus citellus isolate S117 c...	44	0.001
gb AF157839.1 AF157839	Spermophilus elegans elegans isolate...	44	0.001
gb AF030497.1 AF030497	Crocridura brunnea cytochrome b (cyt ...	44	0.001
gb U03541.2 LAU03541	Lenoxus apicalis cytochrome b gene, pa...	44	0.001
gb AF009951.2 AF009951	Heros appendiculatus cytochrome b (c...	44	0.001
gb AF009941.1 AF009941	Tomocichla tuba cytochrome b (cytb) ...	44	0.001
gb AF009925.1 AF009925	Archocentrus sajica cytochrome b (cy...	44	0.001
gb AF094633.1 AF094633	Stachyris whiteheadi cytochrome b ge...	44	0.001
gb AF094621.1 AF094621	Eminia lepida cytochrome b gene, par...	44	0.001
gb AF094618.1 AF094618	Hypergerus atriceps cytochrome b gen...	44	0.001
gb AF166348.1 AF166348	Phascolarctos cinereus cytochrome b ...	44	0.001
gb AF158697.1 AF158697	Geomys bursarius ozarkensis cytochro...	44	0.001
gb AF158694.1 AF158694	Geomys bursarius majusculus cytochro...	44	0.001
gb AF158693.1 AF158693	Geomys bursarius bursarius cytochrom...	44	0.001
gb AF158688.1 AF158688	Geomys bursarius missouriensis cytoc...	44	0.001
gb AF100720.1 AF100720	Spermophilus citellus cytochrome b (...	44	0.001
gb AF091632.1 AF091632	Bubalus depressicornis cytochrome b ...	44	0.001
gb AF102815.1 AF102815	Dromiciops gliroides cytochrome b ge...	44	0.001
gb AF102814.1 AF102814	Vombatus ursinus cytochrome b gene, ...	44	0.001
gb AF022065.1	Tragelaphus euryceros cytochrome b (cytb) ge...	44	0.001
gb AF022059.1	Kobus ellipsiprymnus cytochrome b (cytb) gen...	44	0.001
gb AF022058.1	Antilope cervicapra cytochrome b (cytb) gene...	44	0.001
gb AF022057.1	Tragelaphus oryx cytochrome b (cytb) gene, m...	44	0.001
gb AF022054.1	Antidorcas marsupialis cytochrome b (cytb) g...	44	0.001
gb AF016637.1 AF016637	Connochaetes gnou cytochrome b (cytb...	44	0.001
gb U69863.1 PSU69863	Python sebae cytochrome b (cytb) gene,...	44	0.001
gb U69844.1 LTU69844	Lichanura trivirgata cytochrome b (cyt...	44	0.001
gb AF143193.1 AF143193	Epinephelus sp. cytochrome b (cytb) ...	44	0.001
gb AF121222.1 AF121222	Amphiprion ocellaris isolate 8 cytoc...	44	0.001
gb AF096625.1 AF096625	Kobus ellipsiprymnus defassa cytochr...	44	0.001
gb AF096624.1 AF096624	Kobus ellipsiprymnus ellipsiprymnus c...	44	0.001
gb AF081052.1 AF081052	Eulemur rubriventer cytochrome b (cy...	44	0.001
gb AF081049.1 AF081049	Eulemur macaco macaco cytochrome b (...	44	0.001
gb AF081048.1 AF081048	Eulemur fulvus albifrons cytochrome ...	44	0.001
gb AF082063.1 AF082063	Elminia longicauda cytochrome b gene...	44	0.001
emb AJ010957.1 HAJ10957	Hippopotamus amphibius complete mi...	44	0.001
gb U76506.1 CLU76506	Chlamydera lauterbachii cytochrome b g...	44	0.001
gb U76504.1 CCU76504	Chlamydera cerviniventris cytochrome b...	44	0.001
gb U76505.1 ASU76505	Amblyornis subalaris cytochrome b gene...	44	0.001
gb U76503.1 APU76503	Archboldia papuensis cytochrome b gene...	44	0.001
gb U76508.1 AIU76508	Amblyornis inornatus cytochrome b gene...	44	0.001
gb AF034969.1 AF034969	Connochaetes taurinus cytochrome b g...	44	0.001
gb AF051876.1 AF051876	Rhodeus ocellatus cytochrome b (cytb...	44	0.001
gb AF082007.1 AF082007	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF082006.1 AF082006	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF082005.1 AF082005	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF082004.1 AF082004	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF082003.1 AF082003	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF082002.1 AF082002	Vireo plumbeus plumbeus specimen-vou...	44	0.001
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gb AF081988.1 AF081988	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081987.1 AF081987	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081986.1 AF081986	Vireo plumbeus plumbeus specimen-vou...	44	0.001
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gb AF081983.1 AF081983	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081982.1 AF081982	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081981.1 AF081981	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081980.1 AF081980	Vireo plumbeus plumbeus specimen-vou...	44	0.001

gb AF081991.1 AF081991	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb S73150.1 S73150	cytochrome b (Spermophilus richardsonii-...	44	0.001
gb AF012235.1 AF012235	Cryptomys hottentotus natalensis cyt...	44	0.001
gb U53580.1 NCU53580	Nycticebus coucang cytochrome b (cyt b...	44	0.001
gb U53577.1 EFU53577	Eulemur fulvus rufus cytochrome b (cyt...	44	0.001
gb U53576.1 EFU53576	Eulemur fulvus collaris cytochrome b (...	44	0.001
gb U95512.1 ESERCYTB2	Eptesicus serotinus 3' cytochrome b (...	44	0.001
gb U95508.1 PKUHLCTB2	Pipistrellus kuhli 5' cytochrome b (...	44	0.001
gb U17868.1 BTU17868	Budorcas taxicolor taxicolor cytochrom...	44	0.001
gb U17867.1 BTU17867	Budorcas taxicolor bedfordi cytochrome...	44	0.001
gb U17860.1 ODU17860	Ovis dalli cytochrome b gene, mitochon...	44	0.001
gb U17859.1 OCU17859	Ovis canadensis cytochrome b gene, mit...	44	0.001
emb AJ010556.1 ASP010556	Acomys spinosissimus mitochondrial...	44	0.001
gb AF034736.1 AF034736	Capra falconeri cytochrome b (cytb) ...	44	0.001
gb AF034730.1 AF034730	Ovis aries cytochrome b (cytb) gene,...	44	0.001
gb AF034729.1 AF034729	Ovis vignei cytochrome b (cytb) gene...	44	0.001
gb AF034728.1	Ovis dalli dalli cytochrome b (cytb) gene, m...	44	0.001
gb AF034727.1	Ovis ammon darwini cytochrome b (cytb) gene,...	44	0.001
gb AF034724.1 AF034724	Pantholops hodgsoni cytochrome b (cy...	44	0.001
gb AF034722.1 AF034722	Addax nasomaculatus cytochrome b (cy...	44	0.001
gb U72038.1 MMU72038	Monodon monoceros cytochrome b (cytb)...	44	0.001
gb U72037.1 DLU72037	Delphinapterus leucas cytochrome b (Cy...	44	0.001
gb M99455.1 MURMTCYTB	Murexia longicaudata cytochrome b gen...	44	0.001
gb L29055.1 SHPMTDLOOP	Sheep mitochondrial cytochrome b (Cy...	44	0.001
gb AF082047.1 AF082047	Coccyzus americanus cytochrome b gen...	44	0.001
gb AF038286.1 AF038286	Antechinus minimus cytochrome b gene...	44	0.001
gb AF038284.1 AF038284	Antechinus swainsonii cytochrome b g...	44	0.001
gb AF059093.1 AF059093	Anas undulata cytochrome b gene, par...	44	0.001
gb AF059092.1 AF059092	Anas superciliosa rogersi cytochrome...	44	0.001
gb AF059091.1 AF059091	Anas sparsa cytochrome b gene, parti...	44	0.001
gb AF059080.1 AF059080	Anas melleri cytochrome b gene, part...	44	0.001
gb AF059078.1 AF059078	Anas laysanensis cytochrome b gene, ...	44	0.001
gb AF052240.1 AF052240	Anaïretes flavirostris cytochrome b ...	44	0.001
gb AF006240.1 AF006240	Mitrospingus cassinii cytochrome b (...	44	0.001
gb AF006227.1 AF006227	Dacnis cayana cytochrome b (cytb) ge...	44	0.001
gb AF047447.1 AF047447	Oryx leucoryx cytochrome b gene, mit...	44	0.001
gb U07576.1 AHU07576	Antechinus habbema mitochondrion cyto...	44	0.001
gb AF028180.1 AF028180	Urocyon cinereoargenteus cytochrome ...	44	0.001
gb AF028178.1 AF028178	Pseudalopex sechurae cytochrome b (c...	44	0.001
gb AF028170.1 AF028170	Vulpes zerda cytochrome b (cytb) gen...	44	0.001
gb M99454.1 ASWMTSCYTB	Antechinus stuartii cytochrome b gen...	44	0.001
gb M99453.1 ASWMTCYTB	Antechinus swainsonii cytochrome b ge...	44	0.001
gb U23461.1 ANU23461	Antechinus naso cytochrome b gene, mit...	44	0.001
gb U87138.1 TVU87138	Trichosurus vulpecula cytochrome b (cy...	44	0.001
gb U07590.1 PMU07590	Planigale maculata mitochondrion cyto...	44	0.001
emb AJ004326.1 PTAJ4326	Phylloscopus trochilus mitochondria...	44	0.001
gb AF020255.1 AF020255	Cyclura nubila cytochrome b (cytb) g...	44	0.001
emb Y19184.1 LPA19184	Lama pacos complete mitochondrial genome	44	0.001
gb U88862.1	Amphilophus citrinellum cytochrome b (cytb) ge...	44	0.001
gb U88859.1	Thorichthys aureum cytochrome b (cytb) gene, m...	44	0.001
gb U88858.1	Thorichthys cf. aureum cytochrome b (cytb) gen...	44	0.001
gb U88857.1	Herichthys labridens cytochrome b (cytb) gene,...	44	0.001
gb U88856.1	Herichthys carpiatis cytochrome b (cytb) gene,...	44	0.001
emb Y10524.1 MIMROGEN	Macropus robustus complete mitochondri...	44	0.001
gb U81357.1 CSU81357	Chelydra serpentina cytochrome b gene...	44	0.001
gb U81356.1 CLU81356	Chelodina longicollis cytochrome b gen...	44	0.001
gb U75354.1 LUU75354	Leptomys mexicanus cytochrome b gene...	44	0.001
gb U77332.1 GCU77332	Gymnorhinus cyanocephalus cytochrome-b ...	44	0.001
emb Z29573.1 OVMTGNME	Didelphis virginiana complete mitoch...	44	0.001
emb AJ222679.1 BTCYTQ8	Boselaphus tragocamelus mitochondria...	44	0.001
emb AJ222680.1 TSCYTQ8	Tragelaphus spekkii mitochondrial cyto...	44	0.001
emb AJ222685.1 ODCCTQ8	Oryx dammah mitochondrial cytochrome...	44	0.001
gb M22466.1 PMLMTCYTB	Perameles nasuta cytochrome b gene, c...	44	0.001
gb M22453.1 TQMTCYTB	Thylacinus cynocephalus cytochrome b ...	44	0.001
gb M22450.1 QAVMTCYTB	Dasyurus hallucatus cytochrome b gene...	44	0.001
gb U25737.1 PMU25737	Paradisea minor cytochrome b gene, m...	44	0.001
gb U15203.1 PRU15203	Paradisea rudolphi mitochondrion cyto...	44	0.001
gb U15205.1 EAU15205	Epmachus albertii mitochondrion cyto...	44	0.001
gb U15209.1 PRU15209	Diphyllodes republica mitochondrion c...	44	0.001
emb AJ000424.1 STA424	Sorex tundrensis partial mitochondri...	44	0.001
emb AJ000423.1 STA423	Sorex tundrensis partial mitochondri...	44	0.001

<a href="#">emb AJ000438.1 SIAJ438</a>	Sorex isodon partial mitochondrial c...	44	0.001
<a href="#">emb AJ000437.1 SIAJ437</a>	Sorex isodon partial mitochondrial c...	44	0.001
<a href="#">emb AJ000428.1 SAAJ428</a>	Sorex arcticus partial mitochondrial...	44	0.001
<a href="#">emb AJ000427.1 SAAJ427</a>	Sorex arcticus ssp. maritimensis par...	44	0.001
<a href="#">emb AJ000426.1 SAAJ426</a>	Sorex asper partial mitochondrial cy...	44	0.001
<a href="#">emb AJ000425.1 SAAJ425</a>	Sorex asper partial mitochondrial cy...	44	0.001
<a href="#">emb AJ000418.1 SGAJ418</a>	Sorex granarius partial mitochondria...	44	0.001
<a href="#">emb AJ000417.1 SGAJ417</a>	Sorex granarius partial mitochondria...	44	0.001
<a href="#">emb AJ000416.1 SAAJ416</a>	Sorex araneus partial mitochondrial ...	44	0.001
<a href="#">emb AJ004793.1 HCAJ4793</a>	Hippolais caligata ssp. caligata mi...	44	0.001
<a href="#">emb AJ004792.1 HCAJ4792</a>	Hippolais caligata ssp. rama mitoch...	44	0.001
<a href="#">gb U15718.1 RSU15718</a>	Ramphocelus sanguinolentus cytochrome ...	44	0.001
<a href="#">gb L11905.1 CGYMTCTB3D</a>	Cratogeomys gymnaurus mitochondrial c...	44	0.001
<a href="#">gb U14679.1 POU14679</a>	Philander opossum cytochrome b light s...	44	0.001
<a href="#">gb L11907.1 CGYMTCTB3F</a>	Cratogeomys goldmani rubellus mitoch...	44	0.001
<a href="#">gb L11906.1 CGYMTCTB3E</a>	Cratogeomys merriami mitochondrial c...	44	0.001
<a href="#">gb L11902.1 CGYMTCTB3A</a>	Cratogeomys castanops castanops mito...	44	0.001
<a href="#">emb X92524.1 SLCYTB</a>	S.longirostris cytochrome b gene (compl...	44	0.001
<a href="#">gb U46771.1 ACU46771</a>	Anthus campestris cytochrome b gene, m...	44	0.001
<a href="#">dbj AB021773.1 AB021773</a>	Anguilla interioris mitochondrial c...	44	0.001
<a href="#">dbj AB006953.1 AB006953</a>	Carassius auratus langsdorfi mitoch...	44	0.001
<a href="#">emb Z73492.1 MTPTCTCTB</a>	P.trochilus mitochondrial cytochrome...	44	0.001
<a href="#">dbj AB035239.1 AB035239</a>	Osteoglossum ferreirai mitochondria...	44	0.001
<a href="#">emb X92532.1 MMCCTB2</a>	M.monoceros cytochrome b gene (complet...	44	0.001
<a href="#">emb X74260.1 MIVOCYT3</a>	V.olivaceus mitochondrion gene for cy...	44	0.001
<a href="#">emb X56293.1 MISLCYT3B</a>	S.longirostris mitochondrion cytb gen...	44	0.001
<a href="#">emb X56292.1 MISLCYT3A</a>	S.longirostris mitochondrion cytb ge...	44	0.001
<a href="#">emb X74256.1 MIPVCYT3</a>	P.violaceus mitochondrion gene for cy...	44	0.001
<a href="#">emb X82304.1 MIPHCYT3G</a>	P.hispida mitochondrial cytochrome b...	44	0.001
<a href="#">emb X82302.1 MIPFCYT3G</a>	P.fasciata mitochondrial cytochrome ...	44	0.001
<a href="#">emb X56284.1 MIOACYT3</a>	O.aries mitochondrion cytb gene for c...	44	0.001
<a href="#">emb X74252.1 MIMKCYT3</a>	M.keraudrenii mitochondrion gene for ...	44	0.001
<a href="#">emb X72005.1 MILWCYT3</a>	L.weddelli mitochondrial gene for cyt...	44	0.001
<a href="#">emb X74259.1 MILLCYT3</a>	L.ludovicianus mitochondrion gene for...	44	0.001
<a href="#">emb Y08814.1 MIHLCTB3G</a>	H.liberiensis mitochondrial cytochro...	44	0.001
<a href="#">emb Y08813.1 MIHACYT3</a>	H.amphibius mitochondrial cytochrome ...	44	0.001
<a href="#">emb X56287.1 MIGCCYT3</a>	G.camelopardalis mitochondrion cytb g...	44	0.001
<a href="#">emb X74253.1 MIEFCYT3</a>	E.fastuosus mitochondrion gene for cy...	44	0.001
<a href="#">emb X60941.1 MIEACB3J</a>	Epimachus albertisii mitochondrial ge...	44	0.001
<a href="#">emb X74255.1 MIDMCYT3</a>	D.magnificus mitochondrion gene for c...	44	0.001
<a href="#">emb X56289.1 MICHCTB3</a>	C.hircus mitochondrion cytb gene for ...	44	0.001
<a href="#">emb V00654.1 MI3TXX</a>	Bos taurus complete mitochondrial genome	44	0.001
<a href="#">emb X50940.1 MIAMCB3J</a>	A.macgregoriae mitochondrial gene for...	44	0.001
<a href="#">emb X92530.1 LACYTB</a>	L.albirostris cytochrome b gene (comple...	44	0.001
<a href="#">gb U09265.1 CAU09265</a>	Coccyzus americanus mitochondrion cyto...	44	0.001
<a href="#">dbj AB023906.1 AB023906</a>	Petaurista leucogenys mitochondrial...	44	0.001
<a href="#">dbj AB023905.1 AB023905</a>	Petaurista leucogenys mitochondrial...	44	0.001
<a href="#">dbj AB023904.1 AB023904</a>	Petaurista leucogenys mitochondrial...	44	0.001
<a href="#">dbj AB023903.1 AB023903</a>	Petaurista leucogenys mitochondrial...	44	0.001
<a href="#">dbj D88983.1 D88983</a>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<a href="#">dbj D88638.1 D88638</a>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<a href="#">dbj D88636.1 D88636</a>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<a href="#">dbj D88635.1 D88635</a>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<a href="#">dbj D88633.1 D88633</a>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
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<a href="#">dbj D88630.1 D88630</a>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<a href="#">dbj D88628.1 D88628</a>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<a href="#">dbj D88627.1 D88627</a>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<a href="#">dbj D84204.1 GOTMTC8D</a>	Capra aegagrus mitochondrial DNA for ...	44	0.001
<a href="#">dbj D84202.1 GOTMTC8B</a>	Capra falconeri mitochondrial DNA for...	44	0.001
<a href="#">dbj D82893.1 D82893</a>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<a href="#">dbj D82892.1 D82892</a>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<a href="#">dbj D82891.1 D82891</a>	Bos javanicus mitochondrial DNA for cyt...	44	0.001
<a href="#">dbj Q12121.1 BBUMTC82J</a>	Bubalus arnee bubalis mitochondrial ...	44	0.001
<a href="#">dbj Q14537.1 BBUMTC8A</a>	Bubalus bubalis mitochondrial gene fo...	44	0.001
<a href="#">dbj AB024974.1 AB024974</a>	Capra hircus mitochondrial DNA for ...	44	0.001
<a href="#">dbj AB024973.1 AB024973</a>	Capra hircus mitochondrial DNA for ...	44	0.001
<a href="#">dbj AB024971.1 AB024971</a>	Capra hircus mitochondrial DNA for ...	44	0.001
<a href="#">dbj AB024952.1 AB024952</a>	Capra aegagrus mitochondrial DNA fo...	44	0.001
<a href="#">dbj D88549.1 D88549</a>	Amos depressicollis mitochondrial DNA ...	44	0.001
<a href="#">dbj D88537.1 D88537</a>	Bubalus bubalis mitochondrial DNA for c...	44	0.001



dbj D88634.1 D88634	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj D88631.1 D88631	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj D88629.1 D88629	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj D84205.1 SHPMTCBE	Sheep mitochondrial DNA for cytochrom...	44	0.001
dbj D84203.1 SHPMTCBC	Ovis musimen mitochondrial DNA for cy...	44	0.001
dbj D84201.1 GOTMTCBA	Goat mitochondrial DNA for cytochrome...	44	0.001
dbj D82894.1 D82894	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj D82891.1 D82891	Bubalus quarlesi mitochondrial DNA for ...	44	0.001
dbj D14638.1 BBUMTCBB	Bubalus bubalis mitochondrial gene fo...	44	0.001
dbj D14636.1 BOVMTCCB	Bos javanicus mitochondrial gene for ...	44	0.001
dbj AB017602.1 AB017602	Talpa altaica mitochondrial cytb ge...	44	0.001
dbj AB018985.1 AB018985	Cichlasoma citrinellum mitochondria...	44	0.001
dbj AB004075.1 AB004075	Capra hircus mitochondrial DNA for ...	44	0.001
dbj AB004073.1 AB004073	Capra hircus mitochondrial DNA for ...	44	0.001
dbj AB004070.1 AB004070	Capra hircus mitochondrial DNA for ...	44	0.001
emb X92531.1 DLCTB	D.leucas cytochrome b gene (complete se...	44	0.001
gb U07565.1 HAU07565	Hippopotamus amphibius mitochondrion c...	44	0.001
gb U10367.1 PVU10367	Ptilonorhynchus violaceus mitochondrio...	44	0.001
gb U10364.1 CMU10364	Chlamydera maculata mitochondrion cyto...	44	0.001
emb Z96068.1 ASZ96068	Acomys spinosissimus DNA for mitochon...	42	0.005
gb U76507.1 AIU76507	Amblyornis inornatus cytochrome b gene...	40	0.021
gb AF157466.1 AF157466	Lepus timidus cytochrome b (Cyb) gen...	40	0.021
gb AF157464.1 AF157464	Lepus corsicanus haplotype 1 cytochr...	40	0.021
gb AF157463.1 AF157463	Lepus corsicanus haplotype 3 cytochr...	40	0.021
gb AY016019.1 AY016018S3	Mullerornis agilis cytochrome b ge...	40	0.021
gb AF027330.1	Akodon olivaceus canescens museum catalog nu...	40	0.021
gb AF027329.1	Akodon olivaceus canescens museum catalog nu...	40	0.021
gb AF027328.1	Akodon olivaceus canescens museum catalog nu...	40	0.021
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gb AF027323.1	Akodon olivaceus canescens museum catalog nu...	40	0.021
gb AF027322.1	Akodon olivaceus beatus museum catalog numbe...	40	0.021
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gb AF027311.1	Akodon olivaceus brachiotis museum catalog n...	40	0.021
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gb AF027307.1	Akodon olivaceus brachiotis museum catalog n...	40	0.021
gb AF266188.1 AF266188	Gillichthys mirabilis cytochrome b m...	40	0.021
gb AF324034.1 AF324034	Phyllobates aurotaenia isolate Quebr...	40	0.021
gb AF272639.1 AF272639	Clethrionomys gapperi specimen-vouch...	40	0.021
gb AF272636.1 AF272636	Clethrionomys gapperi specimen-vouch...	40	0.021
gb AF272634.1 AF272634	Clethrionomys gapperi specimen-vouch...	40	0.021
gb AF272633.1 AF272633	Clethrionomys gapperi specimen-vouch...	40	0.021
gb AF182711.1 AF182711	Geopelia cuneata cytochrome b gene. ...	40	0.021
gb AF182587.1 AF182587	Columbina picui cytochrome b gene. P...	40	0.021
gb AF155422.1 AF155422	Sigmodon ochrognathus cytochrome b (...	40	0.021
gb AF155400.1 AF155400	Peromyscus pectoralis lacianus cyto...	40	0.021
gb AF155385.1 AF155385	Peromyscus attwateri isolate 1b cyto...	40	0.021
gb AF155384.1 AF155384	Peromyscus attwateri isolate 1a cyto...	40	0.021
gb AF155522.1 AF155522	Sigmodon ochrognathus isolate Arizac...	40	0.021
gb AF155521.1 AF155521	Sigmodon ochrognathus isolate McLiv7...	40	0.021
gb AF155520.1 AF155520	Sigmodon ochrognathus isolate Duran4...	40	0.021
gb AF155519.1 AF155519	Sigmodon ochrognathus isolate Elm8...	40	0.021
gb AF155518.1 AF155518	Sigmodon ochrognathus isolate Bband4...	40	0.021
gb AF133521.1 AF133521	Trachyphonus darnaudii cytochrome b ...	40	0.021
gb AF254947.1 AF254947	Ureus epilaetus cytochrome b gene. co...	40	0.021
gb AF295531.1 AF295531	Podarcis sicula cytochrome b gene. p...	40	0.021
gb AF123705.1 AF123705	Hippocampus zosterae haplotype PK.14...	40	0.021
cazinc 000994.1	Cavia porcellus complete mitochondrial genome	42	0.021

<u>gb AF004572.1 AF004572</u>	Arvicanthus niloticus cytochrome b (...)	<u>40</u>	0.021
<u>gb AF088932.1 AF088932</u>	Sminthopsis psammophila cytochrome b...	<u>40</u>	0.021
<u>gb U62697.1 ORUCYTB2</u>	Oreopholus ruficollis cytochrome b (cy...	<u>40</u>	0.021
<u>gb U62681.1 CACYTB2</u>	Charadrius australis cytochrome b (cyt ...)	<u>40</u>	0.021
<u>gb U62707.1 CVERCYTB2</u>	Charadrius veredus cytochrome b (cytb...	<u>38</u>	0.084
<u>emb AJ004315.1 HCAJ4315</u>	Hippolais caligata mitochondrial cy...	<u>38</u>	0.084

## Alignments

tmpseq_0	1	cctccctagtttgcttagggattgatcg	26
<u>AF189111</u>	797	.....	772
<u>U86834</u>	858	.....	833
<u>AF123633</u>	56	.....	31
<u>AF123617</u>	104	.....	79
<u>AF127202</u>	107	.....	82
<u>AF127194</u>	107	.....	82
<u>AF217828</u>	845	.....	820
<u>AF160578</u>	869	.....	844
<u>AF009931</u>	869	.....	844
<u>AF091629</u>	869	.....	844
<u>AF034967</u>	869	.....	844
<u>AF038290</u>	869	.....	844
<u>U07577</u>	869	.....	844
<u>U81343</u>	791	.....	766
<u>AJ222681</u>	869	.....	844
<u>M99464</u>	869	.....	844
<u>AJ225116</u>	869	.....	844
<u>U25738</u>	872	.....	847
<u>U25736</u>	872	.....	847
<u>U15202</u>	872	.....	847
<u>U15204</u>	872	.....	847
<u>X56290</u>	869	.....	844
<u>X56286</u>	869	.....	844
<u>D88639</u>	869	.....	844
<u>D82890</u>	869	.....	844
<u>AF119261</u>	869	.....	847
<u>AF123615</u>	101	.....	79
<u>AF160603</u>	866	.....	844
<u>U62687</u>	179	.....	157
<u>U62685</u>	179	.....	157
<u>AF022071</u>	866	.....	844
<u>AF022070</u>	866	.....	844
<u>U81317</u>	872	.....	850
<u>U37293</u>	774	.....	752
<u>U37292</u>	774	.....	752
<u>U37291</u>	774	.....	752
<u>AF082055</u>	51	.....	29
<u>U72770</u>	798	.....	776
<u>U07578</u>	869	.....	847
<u>AF011908</u>	187	.....	165
<u>AJ004231</u>	773	.....	751
<u>AJ004230</u>	773	.....	751
<u>AJ004229</u>	773	.....	751
<u>AJ004232</u>	773	.....	751
<u>U88865</u>	850	.....	828
<u>U90001</u>	536	.....	514
<u>U61057</u>	773	.....	751
<u>AB016404</u>	173	.....	151
<u>AB016402</u>	173	.....	151
<u>AB016400</u>	173	.....	151
<u>AB016398</u>	173	.....	151
<u>U12611</u>	774	.....	752
<u>K22519</u>	869	.....	847
<u>L08014</u>	872	.....	850
<u>L08011</u>	872	.....	850
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<u>AF027324</u>	869	.....	850
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<u>AF027320</u>	869	.....	850
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<u>AF027316</u>	869	.....	850
<u>AF027315</u>	869	.....	850
<u>AF027314</u>	869	.....	850
<u>AF027313</u>	869	.....	850
<u>AF027312</u>	869	.....	850
<u>AF027311</u>	869	.....	850
<u>AF027310</u>	869	.....	850
<u>AF027309</u>	869	.....	850
<u>AF027308</u>	869	.....	850
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<u>AF266188</u>	371	.....	352
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<u>AF272634</u>	869	.....	850
<u>AF272631</u>	869	.....	850
<u>AF182711</u>	712	.....	693
<u>AF182687</u>	774	.....	755
<u>AF155422</u>	869	.....	850
<u>AF155409</u>	869	.....	850
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<u>AF155391</u>	869	.....	850
<u>AF155390</u>	869	.....	850

<u>AF155589</u>	869	.....	850
<u>AF155588</u>	869	.....	850
<u>AF121511</u>	771	.....	752
<u>AF264047</u>	869	.....	850
<u>AF206531</u>	771	.....	752
<u>AF192706</u>	863	.....	844
<u>NC 000884</u>	15032	.....	15013
<u>AF004572</u>	869	.....	850
<u>AF088912</u>	869	.....	850
<u>U62697</u>	176	.....	157
<u>U62681</u>	179	.....	160
<u>U62707</u>	179	.....g.....n..	154
<u>AJ004315</u>	773	.....t.....n.....	748

Database: nt

Posted date: Mar 2, 2001 12:20 AM

Number of letters in database: 2,863,827,885

Number of sequences in database: 807,597

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 19068

Number of Sequences: 807597

Number of extensions: 19068

Number of successful extensions: 7580

Number of sequences better than 10.0: 2441

length of query: 26

length of database: 2,863,827,885

effective RSP length: 17

effective length of query: 9

effective length of database: 2,850,098,736

effective search space: 25650888624

effective search space used: 25650888624

T: 0

A: 30

X1: 6 (11.9 bits)

X2: 15 (29.7 bits)

S1: 12 (24.3 bits)

S2: 16 (32.2 bits)

**Table 12.** The other animals belonging to distantly related species analyzed by our primers to demonstrate its universal nature

SN.	Name of the animal
1.	Indian black buck no.1
2.	Indian black buck no 2
3	sheep
4	pig
5	dog
6	chimpanzee (chimss)
7	human (humsk)
8	Hamster
9	crocodile no1
10	crocodile no2
11	turtle no1
12	turtle no2
13	mouse
14	varanus
15	Naga-naga snake
16	Indian elephant
17	hen
18	dugong
19	lizard
20	weaver bird no1
21	weaver bird no2
22	buffalo no1
23	buffalo no 2



## CLAIMS

- 1 Universal primers named as 'mcb 398' and 'mcb 869' capable of amplifying a fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and revealing the identity of the biological material of any animal of unknown origin at species and sub-species level, said primers, having the sequences:

primers name	Sequence (5'-3')
mcb 398	"TACCATGAGGACAAATATCATTCTG"
mcb 869	"CCTCCTAGTTTGTAGGGATTGATCG"

2. Primers as claimed in claim 1 wherein the fragment of mitochondrial cytochrome b gene is capable of significantly discriminating amongst various evolutionary lineages of different animal species.
3. Primers as claimed in claim 1 wherein the fragment of mitochondrial cytochrome b gene is flanked by the highly conserved sequences amongst a vast range of animal species.
4. Primers as claimed in claim 1 wherein the fragment on mitochondrial cytochrome b gene which is polymorphic inter-specifically, but monomorphic at intra species sources.
5. Primers as claimed in claim 1 wherein in *Antilope cervicapra* species, the sequences of the fragment mentioned under claim 1 are as follows:
- Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra*:
- "taccatgaggacaaatatcttttgaggagcaacagtcacccaatctccttcagcaatcccatacatcggtacaaacctag tagaatgaatctgaggagggtctcagtagataaagcaacccttaccgattttcgccttcactttatcctccatttatcattgc agcccttaccatagtagacactactgtttctccacgaaacaggatccaacaacccacaggaatctcatcagacgcagacaaa attccattccacccctactacactatcaagatatcttaggagctctactattaattttaaccctcatgcttctagtctattctcacc ggacctgcttgagacccagacaactataccagcaaacccacttaatacacccccacatatcaagcccgaatgatacttc ctatttgcatagcaatcctccgatcaattcctaacaactaggagg"
6. A method for the identification of the animal from a biological sample, said method comprising the steps of:
- isolating and amplifying the DNA from the biological sample to be tested using the primers as claimed in claim 1,
  - sequencing the amplified products,
  - blasting the sequence resolved in step (b) against mito database of National Centre for Biotechnology Information (NCBI) using BLAST program and determining the most likely family of the animal source of the biological sample,

- d) blasting the sequence resolved in step (b) against non-redundant (nr) database of National Centre for Biotechnology Information (NCBI) using BLAST program and determining the most likely genus, species or more precisely the sub-species of the animal source of the biological sample,
- 5 e) identifying the most significant alignment of the sequence resolved with cytochrome b gene sequence of the animal identified in steps (c) and (d) respectively and selection of these animals as 'reference animals' for further studies,
- f) isolating and amplifying and sequencing the DNA sequences from the reference animal on both strands in triplicate using the primers as claimed in claim 1,
- 10 g) aligning the sequences obtained using CLUSTAL program and identifying the variable sites amongst the animals analyzed,
- h) comparing the nucleotide sequences pair-wise to determine the variation among the animals resolved and identifying the nucleotide sequence to which the DNA sequence of the biological sample bears maximum similarity as the source animal of the biological sample.
- 15
7. A method as claimed in claim 6 wherein the universal PCR protocol works universally with the DNA template of any unknown animal origin and the universal primers mentioned under column 4.
- 20
8. A method as claimed in claim 6 wherein the Amplification reactions should be carried out in 20  $\mu$ l reaction volume containing approximately 20 ng of template DNA, 100 $\mu$ m each of dNTPs, 1.25 pmole of each primer, 1.5mM MgCl<sub>2</sub>, 0.5 unit of AmpliTaq Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer (10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed should be: an initial denaturation at 95<sup>o</sup>C for 10 min, followed by 35 cycles each of denaturation at 95<sup>o</sup>C for 45 s, annealing at 51<sup>o</sup>C for 1 min, and extension at 72<sup>o</sup>C for 2 min. The extension step at 35<sup>th</sup> cycles should be held for 10 min.
- 25
9. A method as claimed in claim 6 wherein the method enables identification of species of analyzed material (i.e. the DNA isolated from confiscated animal remain of unknown origin) using the public databases such as GenBank, NCBI etc.
- 30
10. A method as claimed in claim 6 wherein the method is used for animal identification to establish the crime with the criminal beyond a reasonably doubt.
11. A method as claimed in claim 6 wherein the method is used to establish the identity of

biological materials such as skin, horns etc confiscated from animal poachers, if it is that of an endangered species.

12. A method as claimed in claim 6 wherein the method is used for establishment of the identity of confiscated animal parts and products of endangered animal species for the purpose of production of molecular evidence of animal hunting and related crime in the court of law, so that the human violation of the wildlife resources could be controlled.
13. A method as claimed in claim 6 wherein the method is used to have an idea of the geographical location of the commitment of wildlife crime based on the cytochrome b gene haplotype of poached animal identified by the universal primer invented.
14. A method as claimed in claim 6 wherein the method is used for animal identification to detect the adulteration of animal meat in food products for the purpose of food fortification, by the food fortification agencies.
15. A method as claimed in claim 6 wherein the method is used to provide a universal technique for detection of the origin of blood or blood stains etc collected from the scene of crime related to offences such as murder, rape etc, in order to establish the origin of blood found at scene of crime when it sounds as if criminals have wantedly spread the blood of an animal at the scene of crime, to confuse the crime investigation agencies and forensic scientists with human blood.
16. A method as claimed in claim 6 wherein the method is used so that it can be converted to a (a) COMMERCIAL 'MOLECULAR KIT' and (b) 'DNA CHIPS' based applications for wildlife identification in forensics.

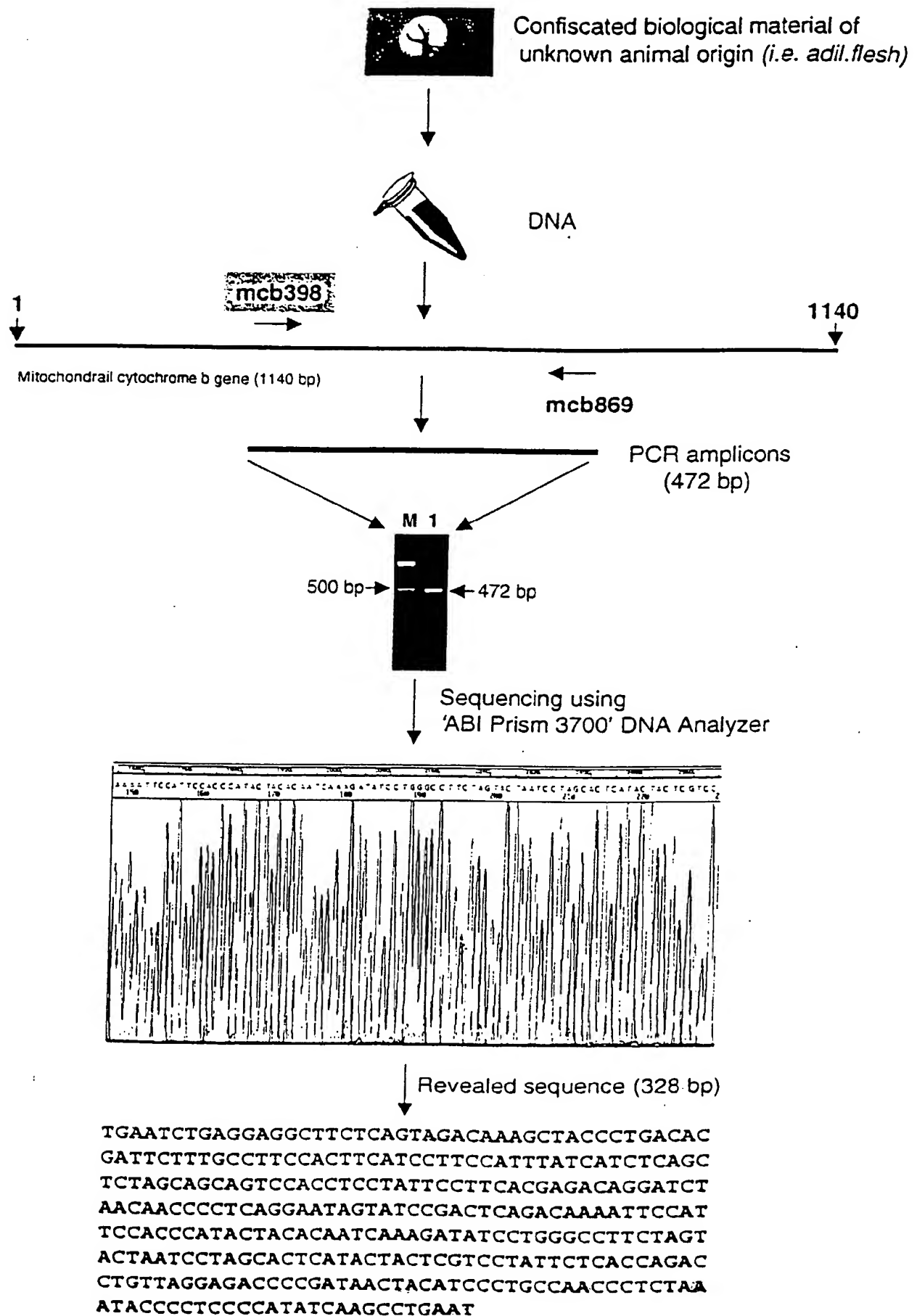
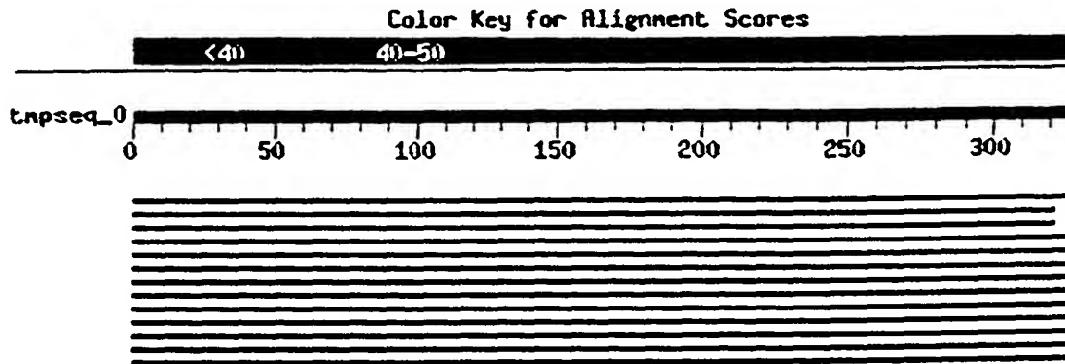


Figure 1 a

Sequence of cytochrome b gene (328 bp) revealed from biological material of unknown origin i.e. '*adil.flesh*' using primers 'mcb398' and 'mcb869'

Homology search in 'nr' database using 'BLAST'

<http://www.ncbi.nlm.nih.gov/BLAST/>



Sequences producing significant alignments:	Score (bits)	E Value
gb AY005809.1  <i>Panthera pardus</i> cytochrome b gene, partial c...	603	e-170
gb AF053054.1 AF053054 <i>Panthera tigris sumatrae</i> isolate Su1...	527	e-147
gb AF053053.1 AF053053 <i>Panthera tigris tigris</i> isolate B7 mi...	527	e-147
gb AF053050.1 AF053050 <i>Panthera tigris corbetti</i> isolate C2 ...	476	e-132
gb AF053049.1 AF053049 <i>Panthera tigris corbetti</i> isolate C1 ...	476	e-132

Selection of reference animals based on above information  
and further analysis using primers 'mcb398' and 'mcb869'

Multiple sequence alignments  
using 'Autoassembler'

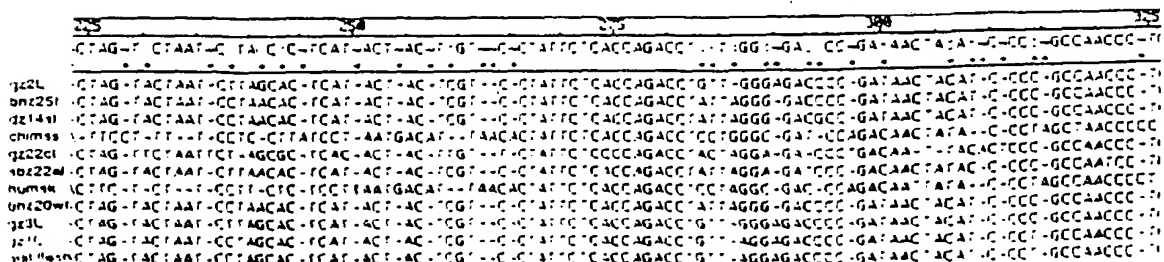


Figure 1 b

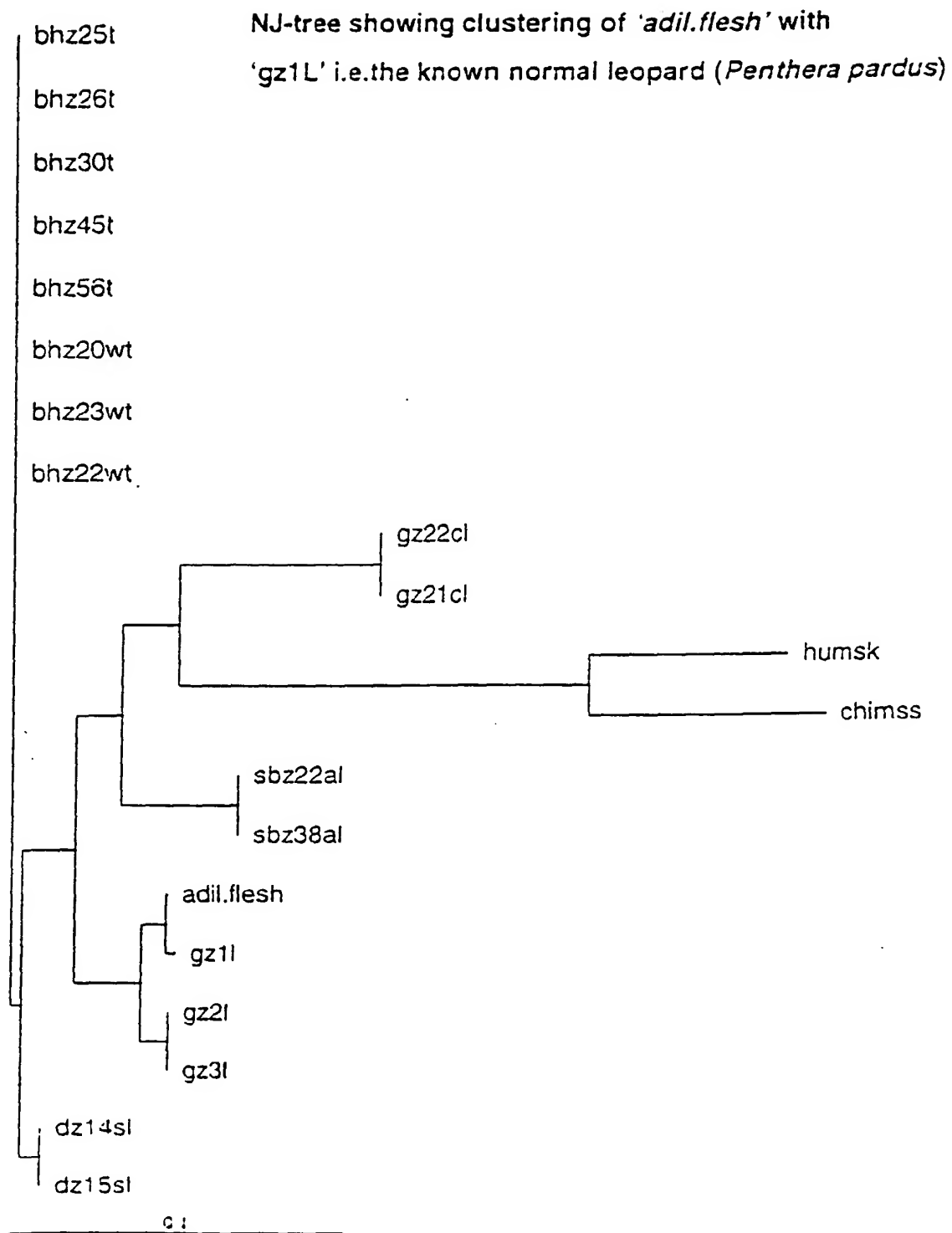


Figure 1c

4/6



Figure 2

5/6

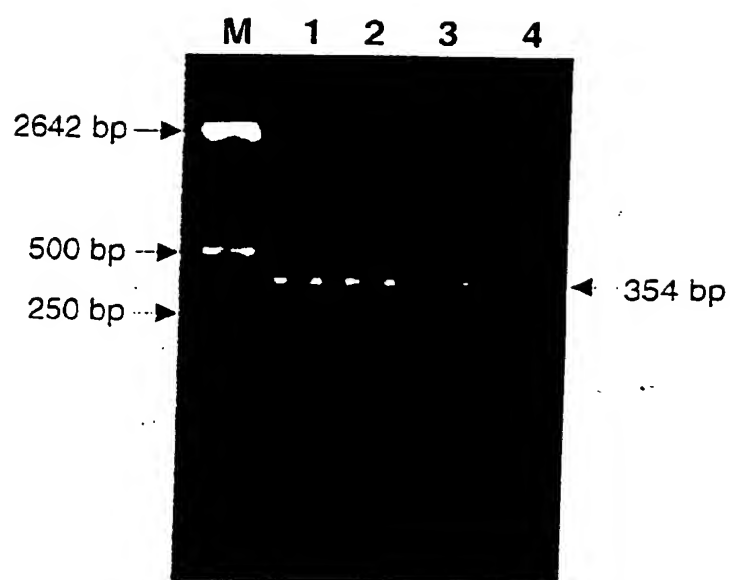


Figure 3



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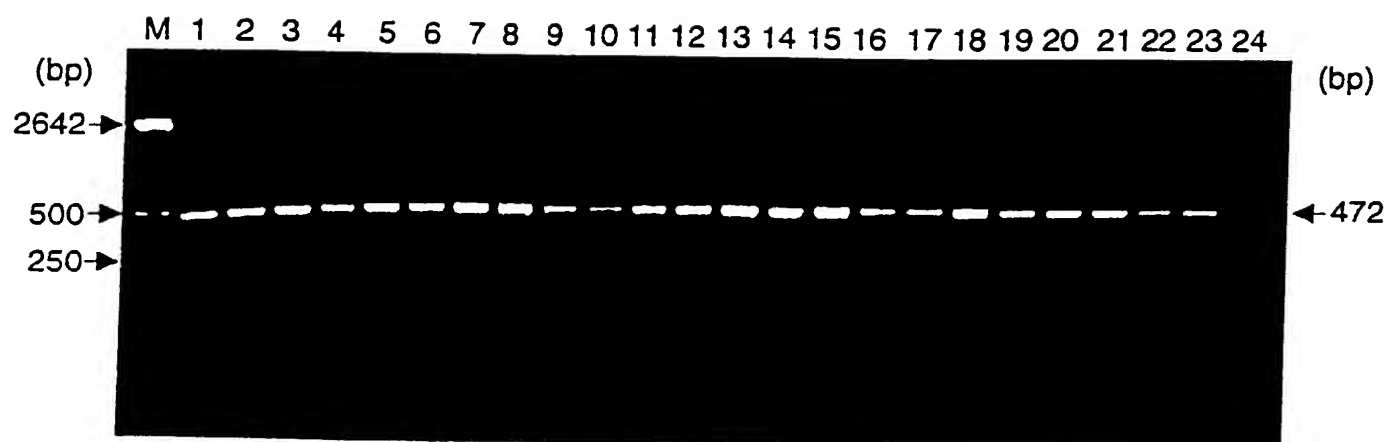


Figure 4

## INTERNATIONAL SEARCH REPORT

Inte Application No

PCT/IN 01/00055

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

BIOSIS, EPO-Internal, EMBL, WPI Data, PAJ, MEDLINE, EMBASE

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	KOCHER T D ET AL: "DYNAMICS OF MITOCHONDRIAL DNA EVOLUTION IN ANIMALS AMPLIFICATION AND SEQUENCING WITH CONSERVED PRIMERS" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES, vol. 86, no. 16, 1989, pages 6196-6200, XP002189444 1989 ISSN: 0027-8424 the whole document	1-16
Y	WO 92 05277 A (DAVIDSON WILLIAM SCOTT ;BARTLETT SYLVIA ERNESTINE (CA)) 2 April 1992 (1992-04-02) the whole document	1-16

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

## ° Special categories of cited documents:

- \*A\* document defining the general state of the art which is not considered to be of particular relevance
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- \*O\* document referring to an oral disclosure, use, exhibition or other means
- \*P\* document published prior to the international filing date but later than the priority date claimed

- \*T\* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- \*X\* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- \*Y\* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- \*G\* document member of the same patent family

Date of the actual completion of the international search

28 February 2002

Date of mailing of the international search report

12/03/2002

Name and mailing address of the ISA

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Authorized officer

Hagenmaier, S

## INTERNATIONAL SEARCH REPORT

International Application No.

PCT/JP 01/00055

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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Y	MATTHEE CONRAD A ET AL: "Cytochrome b phylogeny of the family Bovidae: Resolution within the Alcelaphini, Antilopini, Neotragini, and Tragelaphini." MOLECULAR PHYLOGENETICS AND EVOLUTION, vol. 12, no. 1, June 1999 (1999-06), pages 31-46, XP001053239 ISSN: 1055-7903 the whole document ----	1-16
Y	SHANKARANARAYANAN PATTABHIRAMAN ET AL: "Mitochondrial DNA sequence divergence among big cats and their hybrids." CURRENT SCIENCE (BANGALORE), vol. 75, no. 9, 10 November 1998 (1998-11-10), pages 919-923, XP001063942 ISSN: 0011-3891 the whole document ----	1-16
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Int. Application No

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			WO 9743618 A2	20-11-1997
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